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Entry information

Entry name **FLB2_CAMJE**
 Primary accession number **P22252**
 Secondary accession numbers None
 Entered in Swiss-Prot in Release 19, August 1991
 Sequence was last modified in Release 34, October 1996
 Annotations were last modified in Release 44, July 2004

Name and origin of the protein

Protein name **Flagellin B**
 Synonyms None
 Gene name **Name: flaB**
 From Campylobacter jejuni [TaxID: [197](#)]
 Taxonomy Bacteria; Proteobacteria; Epsilonproteobacteria;
Campylobacterales; Campylobacteraceae; Campylobacter.

References

- [1] SEQUENCE FROM NUCLEIC ACID.
STRAIN=81116;
MEDLINE=91009243;PubMed=2211662 [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]
Nuijten P.J., van Asten F.J., Gaastra W., van der Zeijst B.A.;
 "Structural and functional analysis of two Campylobacter jejuni flagellin genes.";
J. Biol. Chem. 265:17798-17804(1990).

Comments

- **FUNCTION:** Flagellin is the subunit protein which polymerizes to form the filaments of bacterial flagella.
- **SUBUNIT:** Heteropolymer of flaA and flaB.
- **SIMILARITY:** Belongs to the bacterial flagellin family.

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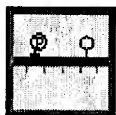
Cross-references

EMBL J05635; AAA23025.1; -. [[EMBL](#) / [GenBank](#) / [DDBJ](#)] [[CoDingSequence](#)]
 PIR B39228; B39228.
 InterPro [IPR001029](#); Flagellin_C.
[IPR010810](#); Flagellin_IN.
[IPR001492](#); Flagellin_N.
[Graphical view of domain structure.](#)
 Pfam [PF00700](#); Flagellin_C; 1.
[PF07196](#); Flagellin_IN; 2.
[PF00669](#); Flagellin_N; 1.
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 ProtoMap [P22252](#).
 PRESAGE [P22252](#).
 DIP [P22252](#).
 ModBase [P22252](#).
 SMR [P22252](#); D0531AF308A7BF1D.
 SWISS-2DPAGE [Get region on 2D PAGE.](#)
 UniRef [View cluster of proteins with at least 50% / 90% identity.](#)

Keywords

Flagellum.

Features



[Feature table viewer](#)

Key	From	To	Length	Description
INIT_MET	0	0		By similarity.

Sequence information

Length: **575** Molecular weight: **59728** CRC64: **D0531AF308A7BF1D** [This is a checksum on the
 AA Da sequence]

10	20	30	40	50	60
GFRINTNIGA	LNAHANSVVN	SNELDKSLSR	LSSGLRINSA	ADDASGMAIA	DSLRSQAATL
70	80	90	100	110	120
GQAINNGNDA	IGILQTADKA	MDEQLKILDT	IKTKATQAAQ	DGQSLKTRTM	LQADINRLME
130	140	150	160	170	180
ELDNIANTTS	FNGKQLLSGN	FTNQEFQIGA	SSNQTIKATI	GATQSSKIGV	TRFETGAQSF
190	200	210	220	230	240

```

TSGVVGLTIK| NYNGIEDFKF| DNVVISTSVG| TGLGALAEI| NKSADKTGVR| ATYDVKTG|
250      260      270      280      290      300
YAIKEGTTSQ| DFAINGVVIG| QINYKGDGNN| GQLVSAINAV| KDTTGVQASK| DENGKLVLT|
310      320      330      340      350      360
ADGRGIKITG| DIGVGSGLA| NQKENYGRSL| LVKNDGRDIN| ISGTNLSAIG| MGTDMISQS|
370      380      390      400      410      420
SVSLRESKGQ| ISATNADAMG| FNSYKGGGKF| VFTQNVSSIS| AFMSAQGSGF| SRGSGFSVGS|
430      440      450      460      470      480
GKNLSVGLSQ| GIQIISSAAS| MSNTYVVSAG| SGFSSGSGNS| QFAALKTTAA| NTTDETAGVT|
490      500      510      520      530      540
TLKGAMAVMD| IAETAITNLD| QIRADIGSVQ| NQLQVTINNI| TVTQVNVKAA| ESTIRDVDFA|
550      560      570
SESANFSKYN| ILAQSGSYAM| SQRNAVQQNV| LKLLQ

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Search Results - Record(s) 1 through 12 of 12 returned.

☐ 1. Document ID: US 6413523 B1

L3: Entry 1 of 12

File: USPT

Jul 2, 2002

DOCUMENT-IDENTIFIER: US 6413523 B1

TITLE: Pharmaceutical composition of escherichia coli heat-labile enterotoxin adjuvant and methods of use

Detailed Description Paragraph Table (1):

TABLE 6 Adjuvant Administered With Campylobacter Antigen Confers Protection Against Against Subsequent Challenge Rabbits Rabbits Colonization Number immunized with challenged with.sup.1 (days + S.D.) resistant.sup.2 -- VC167 8.1 + 1.2 0/6 3 (OA) VC167 8.0 + 1.0 0/7 3 (SON).sup.3 VC167 7.0 + 1.0 1/8 3 (SON + OA) VC167 2.7 + 2.4 9/11 3 (SON) + 1 (OA) VC167 8.0 + 0.8 0/4 -- 81116 7.6 + 0.6 1/3 3 (SON + OA) 81116 6.0 + 1.0 1/4 .sup.1 VC167 is a Lior 8 strain of C. coli and 81116 is a Lior 6 strain of C. jejuni .sup.2 Number of animals negative for Campylobacter 5 days after RITARD challenge/total number in group .sup.3 Sonicates (SON) used for immunization were prepared from VC167

Full

Title

Citation

Front

Review

Classification

Date

Reference

Claims

KWIC

Draw D

☐ 2. Document ID: US 6221582 B1

L3: Entry 2 of 12

File: USPT

Apr 24, 2001

DOCUMENT-IDENTIFIER: US 6221582 B1

TITLE: Polynucleic acid sequences for use in the detection and differentiation of prokaryotic organisms

Detailed Description Text (8):

At present a few PCR assays for the detection of Campylobacter in food, environmental and clinical samples have been described. Oyofe et al. (1992) developed a PCR based on the 5' end of the flaA gene of C. coli VC167. Wegmuller et al. (1993) designed a PCR assay based on the intergenic sequence between the flagellin genes flaA and flaB. Stonnet & Guesdon (1993) developed a PCR test specific for C. jejuni, based on a DNA fragment isolated from a C. jejuni CIP70.2 cosmid library. Van Camp et al. (1993) used the 16S rRNA gene and described a PCR assay that could not discriminate between the different thermophilic Campylobacter species. Eysers et al. (1993), however, developed a Campylobacter species-specific PCR assay based on the region located between helices 43 and 69 of the 23S rRNA.

3. Document ID: US 6083683 A

File: USPT

Jul 4, 2000

TITLE: Methods for detecting shigella bacteria or antibodies to shigella bacteria with an immunoassay

It should be further noted that strains of Lior serotype 8 are of a different species, Campylobacter coli. One of the 2 strains (VC167) of this serotype strongly agglutinated (3+) in anti-81-176 immune rabbit mucus. This result indicates that a vaccine derived from a *C. jejuni* strain (e.g., Lior 5), not only can cross-protect against heterologous serotypes within the same species, but also other Campylobacter species (e.g., Campylobacter coli). Also worth noting is that Lior serotypes 1, 2, 4, 9, and 11 are among the most prevalent disease-associated serotypes world-wide. They all demonstrated detectable cross-reactivity in this assay.

TABLE 16 Agglutination Response of 20
Campylobacter Serotypes Grown Conventionally (BHI-YE) or According to the Methods of
of the Invention (ENHANCED) to Non-immune.sup.b or Anti-81-176.sup.a Immune Rabbit
Mucus Agglutination response.sup.c Lior Non-immune mucus Immune Mucus Strain
Serotype BHI-YE ENHANCED BHI-YE ENHANCED

```

1 - - - ++ 195 2 - - - .+-. 1 4 - - - +++ 170 5 - - - +++ +++++ 81-176 5 - - +++++ +++++
6 6 - - +++++ +++ 81-116 6 - - + ++ 35 7 - - - + 52 8 - + + ++ VC-167 8 - - + +++
VC-159 8 - - - .+-. - 88 9 - - - .+-. 244 11 - - - .+-. +++ 556 17 - - + - 563 18 - - -
- 544 19 - ++ - ++ 699 21 - - - .+-. ++ 1180 28 - - + + 1982 29 - - - - 910 32 - ++
- ++ 2074 36 - - - HC 36 - + - + 2984 46 - - - - 79171 72 - - -

```

^a The anti81-176 mucus were obtained from rabbits infected with live *C. jejuni* 81176 grown conventionally. ^b The nonimmune mucus were obtained from uninfected rabbits. ^c The agglutination responses range from negative (-), to very weak (.-.-), to very strong (++++).

4. Document ID: US 6077678 A

File: USPT

Jun 20, 2000

TITLE: Methods for detecting Campylobacter bacteria or antibodies to Campylobacter bacteria with an immunoassay

It should be further noted that strains of Lior serotype 8 are of a different

species, Campylobacter coli. One of the 2 strains (VC167) of this serotype strongly agglutinated (3+) in anti-81-176 immune rabbit mucus. This result indicates that a vaccine derived from a C. jejuni strain (e.g., Lior 5), not only can cross-protect against heterologous serotypes within the same species, but also other Campylobacter species (e.g., Campylobacter coli). Also worth noting is that Lior serotypes 1, 2; 4, 9, and 11 are among the most prevalent disease-associated serotypes world-wide. They all demonstrated detectable cross-reactivity in this assay.

Detailed Description Paragraph Table (16):

TABLE 16 _____ Agglutination Response of 20
Campylobacter Serotypes Grown Conventionally (BHI-YE) or According to the Methods of
 of the Invention (ENHANCED) to Non-immune.sup.b or Anti-81-176.sup.a Immune Rabbit
 Mucus Agglutination response.sup.c Lior Non-immune mucus Immune Mucus Strain
 Serotype BHI-YE ENHANCED BHI-YE ENHANCED _____ 134
 1 - - - ++ 195 2 - - - .+-. 1 4 - - - +++ 170 5 - - - +++ +++++ 81-176 5 - - - +++++ +++++
 6 6 - - - +++++ +++++ 81-116 6 - - - + ++ 35 7 - - - + 52 8 - + + ++ VC-167 8 - - - + +++++
VC-159 8 - - - .+-. - 88 9 - - - .+-. 244 11 - - - .+-. +++++ 556 17 - - - + - 563 18 - - - -
 - 544 19 - ++ - ++ 699 21 - - - .+-. ++ 1180 28 - - - + +++++ 1982 29 - - - - 910 32 - ++
 - ++ 2074 36 - - - - HC 36 - + - + 2984 46 - - - - 79171 72 - - - -

_____.sup.a The anti81-176 mucus were obtained from rabbits infected with live C. jejuni 81176 grown conventionally .sup.b The nonimmune mucus were obtained from uninfected rabbits .sup.c The agglutination responses range from negative (-), to very weak (.+-), to very strong (++++)

CLAIMS:

4. The method according to claim 3, wherein said Campylobacter bacterium is a Campylobacter jejuni strain selected from the group consisting of 134, 195, 170, 81-81-176, 6, 81-116, 35, 52, VC-167, 88, 244, 544, 699, 1180, 910, and HC.

11. The method according to claim 10 wherein said Campylobacter bacterium is a Campylobacter jejuni strain selected from the group consisting of 134, 195, 170, 81-81-176, 6, 81-116, 35, 52, VC-167, 88, 244, 544, 699, 1180, 910, and HC.

18. The diagnostic immunoassay kit according to claim 17, wherein said Campylobacter bacterium is a Campylobacter jejuni strain selected from the group consisting of 134, 195, 170, 81-176, 6, 81-116, 35, 52, VC-167, 88, 244, 544, 699, 1180, 910, and HC.

Full	Title	Citation	Front	Review	Classification	Date	Reference	Claims	KWIC	Draw D
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☐ 5. Document ID: US 6051416 A

L3: Entry 5 of 12

File: USPT

Apr 18, 2000

DOCUMENT-IDENTIFIER: US 6051416 A

TITLE: Methods for producing enhanced antigenic Helicobacter sp.

Detailed Description Text (161):

It should be further noted that strains of Lior serotype 8 are of a different species, Campylobacter coli. One of the 2 strains (VC167) of this serotype strongly agglutinated (3+) in anti-81-176 immune rabbit mucus. This result indicates that a

vaccine derived from a *C. jejuni* strain (e.g., Lior 5), not only can cross-protect against heterologous serotypes within the same species, but also other *Campylobacter* species (e.g., *Campylobacter coli*). Also worth noting is that Lior serotypes 1, 2, 4, 9, and 11 are among the most prevalent disease-associated serotypes world-wide. They all demonstrated detectable cross-reactivity in this assay.

Detailed Description Paragraph Table (16):

TABLE 16 Agglutination Response of 20
Campylobacter Serotypes Grown Conventionally (BHI-YE) or According to the Methods of
of the Invention (ENHANCED) to Non-immune.sup.b or Anti-81-176.sup.a Immune Rabbit
Mucus Agglutination response.sup.c Lior Non-immune mucus Immune Mucus Strain
 Serotype BHI-YE ENHANCED BHI-YE ENHANCED 134
 1 - - - ++ 195 2 - - - .+-. 1 4 - - - +++ 170 5 - - - +++ +++++ 81-176 5 - - - +++ +++++
 6 6 - - +++++ +++ 81-116 6 - - + ++ 35 7 - - - + 52 8 - + + ++ VC-167 8 - - + +++
 VC-159 8 - - .+-. - 88 9 - - - .+-. 244 11 - - .+-. +++ 556 17 - - + - 563 18 - - -
 - 544 19 - ++ - ++ 699 21 - - .+-. ++ 1180 28 - - + +++ 1982 29 - - - - 910 32 - ++
 - ++ 2074 36 - - - - HC 36 - + - + 2984 46 - - - - 79171 72 - - - -
 .sup.a The anti81-176 mucus were obtained
 from rabbits infected with live *C. jejuni* 81176 grown conventionally .sup.b The
 nonimmune mucus were obtained from uninfected rabbits .sup.c The agglutination
 responses range from negative (-), to very weak (.+-), to very strong (++++)

Full	Title	Citation	Front	Review	Classification	Date	Reference	Claims	KWIC	Draw D
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☐ 6. Document ID: US 5976525 A

L3: Entry 6 of 12

File: USPT

Nov 2, 1999

DOCUMENT-IDENTIFIER: US 5976525 A

TITLE: Method for producing enhanced antigenic enteric bacteria

Detailed Description Text (128):

It should be further noted that strains of Lior serotype 8 are of a different species, *Campylobacter coli*. One of the 2 strains (VC167) of this serotype strongly agglutinated (3+) in anti-81-176 immune rabbit mucus. This result indicates that a vaccine derived from a *C. jejuni* strain (e.g., Lior 5), not only can cross-protect against heterologous serotypes within the same species, but also other *Campylobacter* species (e.g., *Campylobacter coli*). Also worth noting is that Lior serotypes 1, 2, 4, 9, and 11 are among the most prevalent disease-associated serotypes world-wide. They all demonstrated detectable cross-reactivity in this assay.

Detailed Description Paragraph Table (16):

TABLE 16 Agglutination Response of 20
Campylobacter Serotypes Grown Conventionally (BHI-YE) or According to the Methods of
of the Invention (ENHANCED) to Non-immune.sup.b or Anti-81-176.sup.a Immune Rabbit
Mucus Agglutination response.sup.c Lior Non-immune mucus Immune Mucus Strain
 Serotype BHI-YE ENHANCED BHI-YE ENHANCED 134
 1 - - - ++ 195 2 - - - .+-. 1 4 - - - +++ 170 5 - - - +++ +++++ 81-176 5 - - - +++ +++++
 6 6 - - +++++ +++ 81-116 6 - - + ++ 35 7 - - - + 52 8 - + + ++ VC-167 8 - - + +++
 VC-159 8 - - .+-. - 88 9 - - - .+-. 244 11 - - .+-. +++ 556 17 - - + - 563 18 - - -
 - 544 19 - ++ - ++ 699 21 - - .+-. ++ 1180 28 - - + +++ 1982 29 - - - - 910 32 - ++
 - ++ 2074 36 - - - - HC 36 - + - + 2984 46 - - - - 79171 72 - - - -
 .sup.a The anti81-176 mucus were obtained

from rabbits infected with live C. jejuni 81-176 grown conventionally .sup.b The nonimmune mucus were obtained from uninfected rabbits .sup.c The agglutination responses range from negative (-), to very weak (.-.), to very strong (++++)

Full	Title	Citation	Front	Review	Classification	Date	Reference	Claims	KUMC	Draw. De
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☐ 7. Document ID: US 5897475 A

L3: Entry 7 of 12

File: USPT

Apr 27, 1999

DOCUMENT-IDENTIFIER: US 5897475 A

TITLE: Vaccines comprising enhanced antigenic helicobacter spp.

Detailed Description Text (166):

It should be further noted that strains of Lior serotype 8 are of a different species, Campylobacter coli. One of the 2 strains (VC167) of this serotype strongly agglutinated (3+) in anti-81-176 immune rabbit mucus. This result indicates that a vaccine derived from a C. jejuni strain (e.g., Lior 5), not only can cross-protect against heterologous serotypes within the same species, but also other Campylobacter species (e.g., Campylobacter coli). Also worth noting is that Lior serotypes 1, 2, 4, 9, and 11 are among the most prevalent disease-associated serotypes world-wide. They all demonstrated detectable cross-reactivity in this assay.

Detailed Description Paragraph Table (16):

TABLE 16 Campylobacter Serotypes Grown Conventionally (BHI-YE) or According to the Methods of of the Invention (ENHANCED) to Non-immune.sup.b or Anti-81-176.sup.a Immune Rabbit Mucus Agglutination response.sup.c Lior Non-immune mucus Immune Mucus Strain

Serotype	BHI-YE	ENHANCED	BHI-YE	ENHANCED	134
1	-	-	++	195	2
6	6	-	+	++	35
VC-159	8	-	+	++	699
-	544	19	-	++	21
-	++	2074	36	-	-
					HC
					36
					2984
					46
					79171
					72

.sup.a The anti81-176 mucus were obtained from rabbits infected with live C. jejuni 81176 grown conventionally .sup.b The nonimmune mucus were obtained from uninfected rabbits .sup.c The agglutination responses range from negative (-), to very weak (.-.), to very strong (++++)

Full	Title	Citation	Front	Review	Classification	Date	Reference	Claims	KUMC	Draw. De
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☐ 8. Document ID: US 5869066 A

L3: Entry 8 of 12

File: USPT

Feb 9, 1999

DOCUMENT-IDENTIFIER: US 5869066 A

TITLE: Vaccine containing a campylobacter bacterium having an enhanced antigenic property

Detailed Description Text (166):

It should be further noted that strains of Lior serotype 8 are of a different species, Campylobacter coli. One of the 2 strains (VC167) of this serotype strongly agglutinated (3+) in anti-81-176 immune rabbit mucus. This result indicates that a vaccine derived from a C. jejuni strain (e.g., Lior 5), not only can cross-protect against heterologous serotypes within the same species, but also other Campylobacter species (e.g., Campylobacter coli). Also worth noting is that Lior serotypes 1, 2, 4, 9, and 11 are among the most prevalent disease-associated serotypes world-wide. They all demonstrated detectable cross-reactivity in this assay.

Detailed Description Paragraph Table (16):

TABLE 16 _____ Agglutination Response of 20
Campylobacter Serotypes Grown Conventionally (BHI-YE) or According to the Methods of
 of the Invention (ENHANCED) to Non-immune.sup.b or Anti-81-176.sup.a Immune Rabbit
 Mucus Agglutination response.sup.c Lior Non-immune mucus Immune Mucus Strain

Serotype	BHI-YE	ENHANCED	BHI-YE	ENHANCED		134
1	-	-	++	195	2	-
6	6	-	+	++	35	7
VC-159	8	-	+	++	88	9
-	544	19	-	++	699	21
-	++	2074	36	-	HC	36

.sup.a The anti81-176 mucus were obtained from rabbits infected with live C. jejuni 81176 grown conventionally .sup.b The nonimmune mucus were obtained from uninfected rabbits .sup.c The agglutination responses range from negative (-), to very weak (.-.), to very strong (++++)

Full	Title	Citation	Front	Review	Classification	Date	Reference	Claims	K000C	Draw D
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☐ 9. Document ID: US 5858352 A

L3: Entry 9 of 12

File: USPT

Jan 12, 1999

DOCUMENT-IDENTIFIER: US 5858352 A

TITLE: Vaccine containing a Shigella bacterium having an enhanced antigenic property

Detailed Description Text (167):

It should be further noted that strains of Lior serotype 8 are of a different species, Campylobacter coli. One of the 2 strains (VC167) of this serotype strongly agglutinated (3+) in anti-81-176 immune rabbit mucus. This result indicates that a vaccine derived from a C. jejuni strain (e.g., Lior 5), not only can cross-protect against heterologous serotypes within the same species, but also other Campylobacter species (e.g., Campylobacter coli). Also worth noting is that Lior serotypes 1, 2, 4, 9, and 11 are among the most prevalent disease-associated serotypes world-wide. They all demonstrated detectable cross-reactivity in this assay.

Detailed Description Paragraph Table (16):

TABLE 16 _____ Agglutination Response of 20
Campylobacter Serotypes Grown Conventionally (BHI-YE) or According to the Methods of
 of the Invention (ENHANCED) to Non-immune.sup.b or Anti-81-176.sup.a Immune Rabbit
 Mucus Agglutination response Lior Non-immune mucus Immune Mucus Strain Serotype
 BHI-YE ENHANCED BHI-YE ENHANCED _____ 134 1 - - -

++ 195 2 - - - .+- . 1 4 - - - +++ 170 5 - - +++ +++++ 81-176 5 - - +++++ +++++ 6 6 - -
 +++++ +++++ 81-116 6 - - + ++ 35 7 - - - + 52 8 - + + ++ VC-167 8 - - + +++ VC-159 8 -
 - .+- . - 88 9 - - - .+- . 244 11 - - .+- . +++ 556 17 - - + - 563 18 - - - - 544 19 -
 ++ - ++ 699 21 - - .+- . ++ 1180 28 - - + +++ 1982 29 - - - - 910 32 - ++ - ++ 2074
 36 - - - - HC 36 - + - + 2984 46 - - - - 79171 72 - - - -

.sup.a The anti81-176 mucus were obtained from rabbits infected with live C. jejuni 81-176 grown conventionally .sup.b The nonimmune mucus were obtained from uninfected rabbits .sup.c The agglutination responses range from negative (-), to very weak (.+-), to very strong (++++)

Full	Title	Citation	Front	Review	Classification	Date	Reference	Claims	KMNC	Draw D
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☐ 10. Document ID: US 5681736 A

L3: Entry 10 of 12

File: USPT

Oct 28, 1997

DOCUMENT-IDENTIFIER: US 5681736 A

TITLE: Methods for producing enhanced antigenic shigella bacteria and vaccines comprising same

Detailed Description Text (122):

It should be further noted that strains of Lior serotype 8 are of a different species, Campylobacter coli. One of the 2 strains (VC167) of this serotype strongly agglutinated (3+) in anti-81-176 immune rabbit mucus. This result indicates that a vaccine derived from a C. jejuni strain (e.g., Lior 5), not only can cross-protect against heterologous serotypes within the same species, but also other Campylobacter species (e.g., Campylobacter coli). Also worth noting is that Lior serotypes 1, 2, 4, 9, and 11 are among the most prevalent disease-associated serotypes world-wide. They all demonstrated detectable cross-reactivity in this assay.

Detailed Description Paragraph Table (16):

TABLE 16 Agglutination Response of 20
Campylobacter Serotypes Grown Conventionally (BHI-YE) or According to the Methods of
of the Invention (ENHANCED) to Non-immune.sup.b or Anti-81-176.sup.a Immune Rabbit
Mucus Agglutination response.sup.c Lior Non-immune mucus Immune Mucus Strain
 Serotype BHI-YE ENHANCED BHI-YE ENHANCED 134
 1 - - - ++ 195 2 - - - .+- . 1 4 - - - +++ 170 5 - - +++ +++++ 81-176 5 - - +++++ +++++
 6 6 - - +++++ +++++ 81-116 6 - - + ++ 35 7 - - - + 52 8 - + + ++ VC-167 8 - - + +++
 VC-159 8 - - .+- . - 88 9 - - - .+- . 244 11 - - .+- . +++ 556 17 - - + - 563 18 - - -
 - 544 19 - ++ - ++ 699 21 - - .+- . ++ 1180 28 - - + +++ 1982 29 - - - - 910 32 - ++
 - ++ 2074 36 - - - - HC 36 - + - + 2984 46 - - - - 79171 72 - - - -

Full	Title	Citation	Front	Review	Classification	Date	Reference	Claims	KMNC	Draw D
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☐ 11. Document ID: US 5679564 A

L3: Entry 11 of 12

File: USPT

Oct 21, 1997

DOCUMENT-IDENTIFIER: US 5679564 A

TITLE: Methods for producing enhanced antigenic campylobacter bacteria and vaccines

Detailed Description Text (120):

It should be further noted that strains of Lior serotype 8 are of a different species, Campylobacter coli. One of the 2 strains (VC167) of this serotype strongly agglutinated (3+) in anti-81-176 immune rabbit mucus. This result indicates that a vaccine derived from a C. jejuni strain (e.g., Lior 5), not only can cross-protect against heterologous serotypes within the same species, but also other Campylobacter species (e.g., Campylobacter coli). Also worth noting is that Lior serotypes 1, 2, 4, 9, and 11 are among the most prevalent disease-associated serotypes world-wide. They all demonstrated detectable cross-reactivity in this assay.

Detailed Description Paragraph Table (16):

TABLE 16 Agglutination Response of 20
Campylobacter Serotypes Grown Conventionally (BHI-YE) or According to the Methods of
of the Invention (ENHANCED) to Non-immune.sup.b or Anti-81-176.sup.a Immune Rabbit
Mucus Agglutination response.sup.c Lior Non-immune mucus Immune Mucus Strain
 Serotype BHI-YE ENHANCED BHI-YE ENHANCED 134
 1 - - - ++ 195 2 - - - .+-. 1 4 - - - +++ 170 5 - - - +++ +++++ 81-176 5 - - - +++ +++++
 6 6 - - - +++++ + 81-116 6 - - - + ++ 35 7 - - - + 52 8 - - - + + ++ VC-167 8 - - - + ++
 VC-159 8 - - - .+-. - 88 9 - - - .+-. 244 11 - - - .+-. + 556 17 - - - + - 563 18 - - -
 - 544 19 - - - + + 699 21 - - - .+-. + 1180 28 - - - + + 1982 29 - - - - 910 32 - - - + +
 - + 2074 36 - - - - HC 36 - - - + 2984 46 - - - - 79171 72 - - - -

.sup.a The anti81-176 mucus were obtained from rabbits infected with live C. jejuni 81-176 grown conventionally .sup.b The nonimmune mucus were obtained from uninfected rabbits .sup.c The agglutination responses range from negative (-), to very weak (.+-), to very strong (++++)

CLAIMS:

4. The method according to claim 3, wherein said Campylobacter species is a Campylobacter jejuni strain selected from the group consisting of 134, 195, 170, 81-81-176, 6, 81-116, 35, 52, VC-167, 88, 244, 544, 699, 1180, 910, and HC.

10. The Campylobacter bacterium according to claim 9, wherein said Campylobacter species is a Campylobacter jejuni strain selected from the group consisting of 134, 195, 170, 81-176, 6, 81-116, 35, 52, VC-167, 88, 244, 544, 699, 1180, 910, and HC.

Full	Title	Citation	Front	Review	Classification	Date	Reference	Claims	KNOC	Draw. De
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☐ 12. Document ID: US 5494795 A

L3: Entry 12 of 12

File: USPT

Feb 27, 1996

DOCUMENT-IDENTIFIER: US 5494795 A

TITLE: Specific oligonucleotide primers for detection of pathogenic campylobacter bacteria by polymerase chain reaction

Brief Summary Text (11):

These and additional objects of the invention are accomplished by application of

standard PCR methodology employing the oligonucleotide primers pg50 (5'-ATGGGATTTCTGTTTAAAC-3' (SEQ ID No. 1)) and pg3 (5'-GAACTTGAACCGATTTG-3' (SEQ ID No. 2)) to amplify DNA from the *flaA* flagellin gene of *Campylobacter coli* strain VC167 and the digoxigenin-labeled probe pBA273 to detect the amplified DNA in fecal specimens (extracted by the method of G. Frankel, et al., Mol. Microbiol. 3:1729-1734, 1989) of animals and humans.

Detailed Description Text (4):

Two oligonucleotides, pg50 (5'-ATGGGATTTCTGTTTAAAC-3' (SEQ ID No. 1)) and pg3 (5'-GAACTTGAACCGATTTG-3' (SEQ ID No. 2)), have been selected from the DNA sequence of the *flaA* flagellin gene (base pairs 289-2007, GenBank Accession No. M64670) of *C. coli* strain VC167 (see FIG. 1); pg50 is between base pairs 289-306 and pg3 is between base pairs 730-746 on the minus strand. These two oligonucleotides function as specific primers for PCR amplification of *C. coli* and *C. jejuni* DNA. A probe internal to the amplified gene region was constructed by standard methods (T. Maniatis, et al., Molecular Cloning: A Laboratory Manual. Cold Spring Harbor Lab., Cold Spring Harbor, N.Y., 1982) for detection of the PCR-amplified *Campylobacter* DNA. The probe lies between base pairs 481-759 of the DNA in GenBank Accession No. M64670. The results were reported by poster presentation at the American Society for Microbiology on 30 May 1992 (Abstracts of the General Meeting, D-206, p. 130) and in the J. Clin. Microbiol. 30:2613-2619, 1992, by the inventors, and are described in detail below.

Detailed Description Text (12):

The oligonucleotide primers pg50 (5'-ATGGGATTTCTGTTTAAAC-3' (SEQ ID No. 1)) and pg3 (5'-GAACTTGAACCGATTTG-3' (SEQ ID No. 2)) derived from the well-conserved amino terminus of the *flaA* flagellin gene of *Campylobacter coli* strain VC167 (P. Guerry, et al., J. Bacteriol. 172:1853-1860, 1990; cf. FIG. 1) were selected following comparison of 30 strains of *C. coli* and *C. jejuni* by DNA hybridization (S. A. Thornton, et al., Infect. Immun. 58:2686-2698, 1990) and N-terminal amino acid sequencing of flagella from various strains of *C. coli* and *C. jejuni*. These oligonucleotide sequences represent well-conserved but distinctive DNA sequences in the *flaA* N-termini of both *C. coli* and *C. jejuni* but are not present in DNA sequences of other *Campylobacter* spp. such J. Clinical Microbiology 1992). Primer pg50 binds to the beginning of *flaA* but not *flaB*; primer pg3 binds to the second strand 450 base pairs downstream from the pg50-binding site on *flaA* as well as at the corresponding position of *flaB*.

Detailed Description Text (24):

Using the digoxigenin-labeled pBA273 probe, serial dilutions of DNA extracted from cultured VC167 bacteria were subjected to PCR amplification using the pg3-pg50 primers, and the products were electrophoresed and transferred to a nylon membrane by Southern blotting (T. Maniatis, et al., *ibid*) and hybridized in 533 SSC buffer (1.times.SSC=0.015 M sodium citrate-0.15 M sodium chloride) for 16-24 hr at 60.degree. C. with 230 ng of digoxigenin-labeled probe per 100 cm.sup.2 of membrane. The results indicate that the PCR products generated with as little as 0.062 pg of DNA can be visualized on the agarose gel and that hybridization with the internal probe allows detection of a little as 0.0062 pg of DNA. Based on the genome size for *Campylobacter* spp. of 1,700 kilobase pairs, this corresponds to four four or fewer bacteria.

Detailed Description Text (26):

In order to evaluate the feasibility of direct PCR detection of *campylobacters* in fecal material, rectal swabs were taken from 15 rabbits which were fed VC167 2 days prior to sampling, and from 15 control rabbits which had been fed sterile culture broth. Following transport to the laboratory in Cary Blair medium, aliquots of fecal material from each rabbit were re-suspended in phosphate buffered saline as described above. An aliquot from each sample was plated directly onto *campylobacter* blood agar and the plates were incubated microaerobically for 48 h. Another aliquot was processed for PCR using the extraction method of Frankel et al. (*ibid*), the

products were dot blotted, and hybridized to the non-radioactively labelled internal probe from pBA273. The PCR assay detected *C. coli* in all 15 infected rabbits, although only 12/15 rabbits were positive by plating. No *Campylobacter* were detected in the uninfected control rabbits by either PCR or plating.

Detailed Description Paragraph Table (2):

SEQUENCE LISTING (1) GENERAL INFORMATION: (iii) NUMBER OF SEQUENCES: 2 (2) INFORMATION FOR SEQ ID NO:1: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 18 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (vi) ORIGINAL SOURCE: (A) ORGANISM: *Campylobacter coli* (B) STRAIN: VC167 (x) PUBLICATION INFORMATION: (A) AUTHORS: Oyofe, Buhari A Thornton, Scott A Burr, Donald H. Trust, Trevor J Pavlovskis, Olgerts R Guerry, Patricia (B) TITLE: Specific Detection of *Campylobacter jejuni* and *Campylobacter coli* by Using Polymerase Chain Reaction (C) JOURNAL: J. Clin. Microbiol. (D) VOLUME: 30 (E) ISSUE: 10 (F) PAGES: 2613-2619 (G) DATE: October-1992 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1: ATGGGATTTCGTATTAAC 18 (2) INFORMATION FOR SEQ ID NO:2: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: YES (vi) ORIGINAL SOURCE: (A) ORGANISM: *Campylobacter coli* (B) STRAIN: VC167 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2: GAACTTGAACCGATTG17

Full	Title	Citation	Front	Review	Classification	Date	Reference			Claims	KWIC	Draw. De
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L3: Entry 12 of 12

File: USPT

Feb 27, 1996

DOCUMENT-IDENTIFIER: US 5494795 A

TITLE: Specific oligonucleotide primers for detection of pathogenic campylobacter bacteria by polymerase chain reaction

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L5: Entry 8 of 19

File: USPT

Oct 10, 2000

DOCUMENT-IDENTIFIER: US 6130082 A

TITLE: Recombinant flagellin vaccinesAbstract Text (1):

The present invention is directed to recombinant genes and their encoded proteins which are recombinant flagellin fusion proteins. Such fusion proteins comprise amino acid sequences specifying an epitope encoded by a flagellin structural gene and an epitope of a heterologous organism which is immunogenic upon introduction of the fusion protein into a vertebrate host. The recombinant genes and proteins of the present invention can be used in vaccine formulations, to provide protection against infection by the heterologous organism, or to provide protection against conditions or disorders caused by an antigen of the organism. In a specific embodiment, attenuated invasive bacteria expressing the recombinant flagellin genes of the invention can be used in live vaccine formulations. The invention is illustrated by way of examples in which epitopes of malaria circumsporozoite antigens, the B subunit of Cholera toxin, surface and presurface antigens of Hepatitis B. VP7 polypeptide of rotavirus, envelope glycoprotein of HIV, and M protein of Streptococcus, are expressed in recombinant flagellin fusion proteins which assemble into functional flagella, and which provoke an immune response directed against the heterologous epitope, in a vertebrate host.

Brief Summary Text (16):

Cholera toxin is the prototype of a family of bacterial enterotoxins which mediate diarrheal disease and are related in structure, function and immunogenicity. Other members of this family include the heat-labile toxin of *E. coli* isolated from humans (Yamamoto, T. and Yokota, T., 1983, *J. Bacteriology* 155:728) and from pigs (Leong, J., et al., 1985, *Infect. Immun.* 48:73), and toxins from *Salmonella typhimurium* (Finkelstein, R. A., et al., 1983, *FEMS Microbiology Letters* 17:239) and from *Campylobacter jejuni* (Walker, R. I., et al., 1986, *Microbiology Rev.* 50:81). Common to all of these toxins is an A subunit which mediates ADP-ribosyltransferase activity, resulting in the activation of adenylate cyclase, ultimately leading to death of the target cell. In addition, all of these toxins contain an immunologically dominant B subunit which mediates binding of the holotoxin to the target cell. The B subunit by itself is non-toxic, and immunization with this molecule induces the formation of toxin-neutralizing antibodies.

Brief Summary Text (23):

Flagella are found primarily, although not exclusively, on the surface of rod and spiral shaped bacteria, including members of the genera *Escherichia*, *Salmonella*, *Proteus*, *Pseudomonas*, *Bacillus*, *Campylobacter*, *Vibrio*, *Treponema*, *Legionella*, *Clostridia*, *Caulobacter*, and others. These flagella, although they perform the same function, are polymorphic in molecular weight across genera, ranging from 28-66 kd. A high degree of antigenic polymorphism is seen even within a single genus, such as *Salmonella*, and is useful for identifying individual serotypes within a single species (Edwards, P. R. and Ewing, W. H., 1972, *Identification of Enterobacteriaceae*, 3d ed., Burgess Publishing Co., Minneapolis, Minn.). Structural analyses of several bacterial flagella have revealed a common architecture among

filaments isolated from different bacteria (Wei, L.-N. and Joys, T. M., 1985, J. Mol. Bio. 186:791; DeLange, R. J., et al., 1976, J. Biol. Chem. 251:705; Gill, P. R. R. and Agabian, J., Biol. Chem. 258:7395). Most striking is a high degree of protein sequence homology at the amino and carboxy termini of these molecules, and the presence of a polymorphic central region which is responsible for the antigenic diversity among different flagella.

Detailed Description Text (17):

If the cloned flagellin gene is not readily available, it may be cloned by standard procedures known in the art (see, e.g., Maniatis, T., et al., 1982, Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York), with any flagellated bacterial cell potentially serving as the nucleic acid source for the molecular cloning. Such bacteria include but are not limited to Escherichia, Salmonella, Proteus, Pseudomonas, Bacillus, Campylobacter, Vibrio, Treponema, Legionella, Clostridia, and Caulobacter.

Detailed Description Text (53):

In a specific embodiment, any attenuated bacterial hosts which express the recombinant flagellin can be formulated as live vaccines. Such bacteria include but are not limited to attenuated invasive strains and attenuated Campylobacter, Shigella or Escherichia species.

CLAIMS:

1. A recombinant gene comprising a nucleotide sequence which encodes a flagellin fusion protein, which protein comprises a flagellin sequence containing a first epitope of a Salmonella H1-d flagellin structural gene with at least one epitope of a heterologous organism inserted within the flagellin sequence, wherein the flagellin protein is capable of binding to an anti-flagellin antibody, wherein the DNA encoding at least one epitope of the heterologous organism is inserted in place of the DNA which naturally occurs between the natural EcoRV sites of the Salmonella H1-d gene.

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NCBI BLAST program reference [PMID:9254694]:
Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W., Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. 25:3389-3402(1997).

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Query length: 575 AA (of which 9% low-complexity regions filtered out)
Date run: 2004-08-31 17:39:24 UTC+0100 on sib-gml.unil.ch
Program: NCBI BLASTP 1.5.4-Paracel [2003-06-05]
Database: EXPASY/UniProt
1,544,870 sequences; 494,584,931 total letters

Taxonomic view	NiceBlast view	Printable view
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List of potentially matching sequences

Send selected sequences to

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	Db	AC	Description	Score	E-value
<input type="checkbox"/>	sp	P22251	FLA2_CAMJE Flagellin A [flaA] [Campylobacter jejuni]	983	0.0
<input type="checkbox"/>	tr	O85179	Flagellin A [flaA] [Campylobacter jejuni]	983	0.0
<input type="checkbox"/>	tr	Q9R950	Flagellin A [flaA] [Campylobacter jejuni]	979	0.0
<input type="checkbox"/>	tr	Q9R953	Flagellin A [flaA] [Campylobacter jejuni]	979	0.0
<input type="checkbox"/>	tr	Q9RF26	Chimeric flagellin A/B [Campylobacter jejuni]	977	0.0
<input type="checkbox"/>	tr	O85183	Flagellin A [flaA] [Campylobacter jejuni]	957	0.0
<input type="checkbox"/>	tr	Q8G9F3	Flagellin (Fragment) [flaA] [Campylobacter coli]	956	0.0
<input type="checkbox"/>	tr	Q7X516	FlaB [flaB] [Campylobacter jejuni]	935	0.0
<input type="checkbox"/>	tr	Q9RF25	Flagellin B [flaB] [Campylobacter jejuni]	934	0.0
<input type="checkbox"/>	sp	P22252	FLB2_CAMJE Flagellin B [flaB] [Campylobacter jejuni]	932	0.0

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<input type="checkbox"/>	tr Q99Q27	Flagellin A (Fragment) [flaA] [Campylobacter jejuni]	905	0.0
<input type="checkbox"/>	tr Q99QL6	Flagellin A (Fragment) [flaA] [Campylobacter jejuni]	905	0.0
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<input type="checkbox"/>	tr Q93NL9	Flagellin A (Fragment) [flaA] [Campylobacter jejuni]	874	0.0
<input type="checkbox"/>	sp P27053	FLAA_CAMCO Flagellin A [flaA] [Campylobacter coli]	873	0.0
<input type="checkbox"/>	tr Q84IB9	Flagellin (Fragment) [flaA] [Campylobacter jejuni]	863	0.0
<input type="checkbox"/>	tr Q46009	Flagellin [Campylobacter coli]	848	0.0
<input type="checkbox"/>	sp P18245	FLAB_CAMCO Flagellin B (Flagellin N) [flaB] [Campylobacter jejuni]	837	0.0
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<input type="checkbox"/>	tr Q84IB8	Flagellin (Fragment) [flaA] [Campylobacter jejuni]	802	0.0
<input type="checkbox"/>	tr Q9R952	Flagellin A [flaA] [Campylobacter jejuni]	801	0.0
<input type="checkbox"/>	sp P56963	FLA1_CAMJE Flagellin A [flaA] [Campylobacter jejuni]	800	0.0
<input type="checkbox"/>	tr O85182	Flagellin A [flaA] [Campylobacter jejuni]	796	0.0
<input type="checkbox"/>	tr Q9R949	Flagellin A [flaA] [Campylobacter jejuni]	796	0.0
<input type="checkbox"/>	tr O30696	Flagellin A [flaA] [Campylobacter jejuni]	795	0.0
<input type="checkbox"/>	tr O30689	Flagellin A [flaA] [Campylobacter jejuni]	794	0.0
<input type="checkbox"/>	tr Q8G9F2	Flagellin (Fragment) [flaA] [Campylobacter jejuni]	793	0.0
<input type="checkbox"/>	tr O34938	Flagellin A [flaA] [Campylobacter jejuni]	792	0.0
<input type="checkbox"/>	tr O85180	Flagellin A [flaA] [Campylobacter jejuni]	785	0.0
<input type="checkbox"/>	tr Q8G9F1	Flagellin (Fragment) [flaA] [Campylobacter coli]	782	0.0
<input type="checkbox"/>	sp Q46114	FLB3_CAMJE Flagellin B [flaB] [Campylobacter jejuni]	776	0.0
<input type="checkbox"/>	tr Q8G9F0	Flagellin (Fragment) [flaA] [Campylobacter jejuni]	768	0.0
<input type="checkbox"/>	tr Q79AR6	Flagellin [flaA] [Campylobacter jejuni]	767	0.0
<input type="checkbox"/>	sp P56964	FLB1_CAMJE Flagellin B [flaB] [Campylobacter jejuni]	766	0.0
<input type="checkbox"/>	tr Q6L5K6	Flagellin (Fragment) [flaA] [Campylobacter lari]	766	0.0
<input type="checkbox"/>	tr Q6L5J8	Flagellin (Fragment) [flaA] [Campylobacter lari]	765	0.0
<input type="checkbox"/>	tr Q9R951	Flagellin B [flaB] [Campylobacter jejuni]	763	0.0
<input type="checkbox"/>	tr Q933V4	Flagellin A (Fragment) [flaA] [Campylobacter jejuni]	762	0.0
<input type="checkbox"/>	tr Q6L5K1	Flagellin (Fragment) [flaA] [Campylobacter lari]	762	0.0
<input type="checkbox"/>	tr Q9R954	Flagellin B [flaB] [Campylobacter jejuni]	761	0.0
<input type="checkbox"/>	tr Q6L5J9	Flagellin (Fragment) [flaA] [Campylobacter lari]	761	0.0
<input type="checkbox"/>	tr Q93NL8	Flagellin A (Fragment) [flaA] [Campylobacter jejuni]	760	0.0
<input type="checkbox"/>	tr Q93NL7	Flagellin A (Fragment) [flaA] [Campylobacter jejuni]	756	0.0
<input type="checkbox"/>	tr Q6L5K5	Flagellin (Fragment) [flaA] [Campylobacter lari]	756	0.0
<input type="checkbox"/>	tr Q6L5K8	Flagellin (Fragment) [flaA] [Campylobacter lari]	755	0.0
<input type="checkbox"/>	tr Q6L5J7	Flagellin (Fragment) [flaA] [Campylobacter lari]	755	0.0
<input type="checkbox"/>	tr Q6L5K2	Flagellin (Fragment) [flaA] [Campylobacter lari]	754	0.0
<input type="checkbox"/>	tr Q6L5K9	Flagellin (Fragment) [flaA] [Campylobacter lari]	754	0.0
<input type="checkbox"/>	tr Q6L5L0	Flagellin (Fragment) [flaA] [Campylobacter lari]	754	0.0
<input type="checkbox"/>	tr Q6L5K4	Flagellin (Fragment) [flaA] [Campylobacter lari]	751	0.0
<input type="checkbox"/>	tr Q6L5K7	Flagellin (Fragment) [flaA] [Campylobacter lari]	751	0.0
<input type="checkbox"/>	tr Q6L5J6	Flagellin (Fragment) [flaA] [Campylobacter lari]	749	0.0
<input type="checkbox"/>	tr Q6L5L1	Flagellin (Fragment) [flaA] [Campylobacter lari]	747	0.0
<input type="checkbox"/>	tr O85181	Flagellin B [flaB] [Campylobacter jejuni]	747	0.0

<input type="checkbox"/>	tr	Q6L5K0	Flagellin (Fragment) [flaA] [Campylobacter lari]	746	0.0
<input type="checkbox"/>	tr	Q6L5K3	Flagellin (Fragment) [flaA] [Campylobacter lari]	742	0.0
<input type="checkbox"/>	tr	P96751	Flagellin (Fragment) [flaA] [Campylobacter sp]	605	e-172
<input type="checkbox"/>	tr	P96752	Flagellin [flaB] [Campylobacter sp]	598	e-169
<input type="checkbox"/>	tr	Q84IC4	Flagellin (Fragment) [flaA] [Campylobacter lari]	537	e-151
<input type="checkbox"/>	tr	Q84IC5	Flagellin (Fragment) [flaA] [Campylobacter lari]	534	e-150
<input type="checkbox"/>	tr	Q84IC7	Flagellin (Fragment) [flaA] [Campylobacter lari]	523	e-147
<input type="checkbox"/>	tr	Q84IC8	Flagellin (Fragment) [flaA] [Campylobacter lari]	481	e-134
<input type="checkbox"/>	tr	Q93GT4	Flagellin (Fragment) [flaA] [Campylobacter lari]	476	e-133
<input type="checkbox"/>	tr	Q8RTY4	Flagellin (Fragment) [flaA] [Campylobacter lari]	475	e-132
<input type="checkbox"/>	tr	Q56746	Flagellin [flag] [Wolinella succinogenes]	474	e-132
<input type="checkbox"/>	tr	Q93R24	Flagellin (Fragment) [flaA] [Campylobacter lari]	474	e-132
<input type="checkbox"/>	tr	Q7M7N1	FLAGELLIN B [FLAB] [Wolinella succinogenes]	473	e-132
<input type="checkbox"/>	tr	Q84IC9	Flagellin (Fragment) [flaA] [Campylobacter lari]	471	e-131
<input type="checkbox"/>	tr	Q93GT1	Flagellin (Fragment) [flaA] [Campylobacter lari]	469	e-131
<input type="checkbox"/>	tr	Q84IC3	Flagellin (Fragment) [flaA] [Campylobacter lari]	469	e-131
<input type="checkbox"/>	tr	Q84IC6	Flagellin (Fragment) [flaA] [Campylobacter lari]	468	e-130
<input type="checkbox"/>	tr	Q84IC2	Flagellin (Fragment) [flaA] [Campylobacter lari]	466	e-130
<input type="checkbox"/>	tr	Q93GT2	Flagellin (Fragment) [flaA] [Campylobacter lari]	462	e-129
<input type="checkbox"/>	tr	Q84IC1	Flagellin (Fragment) [flaA] [Campylobacter lari]	462	e-129
<input type="checkbox"/>	tr	Q93GT3	Flagellin (Fragment) [flaA] [Campylobacter lari]	456	e-127
<input type="checkbox"/>	tr	Q46462	Flagellin (Fragment) [fla2] [Campylobacter upsaliensis]	451	e-125
<input type="checkbox"/>	tr	Q46461	Flagellin (Fragment) [fla1] [Campylobacter upsaliensis]	446	e-124
<input type="checkbox"/>	sp	Q9XB38	FLAA_HELFE Flagellin A [flaA] [Helicobacter felis]	444	e-123
<input type="checkbox"/>	tr	Q7X2D1	Flagellin A [flaA] [Helicobacter pylori (Campylobacter...]	443	e-123
<input type="checkbox"/>	sp	Q03843	FLAA_HELPY Flagellin A [flaA] [Helicobacter pylori (Ca...]	438	e-121
<input type="checkbox"/>	tr	Q8GD49	Flagellin [flaB] [Helicobacter pylori (Campylobacter p...]	434	e-120
<input type="checkbox"/>	tr	Q6VYQ2	Flagellin A [flaA] [Helicobacter pylori (Campylobacter...]	433	e-120
<input type="checkbox"/>	tr	Q84IC0	Flagellin (Fragment) [flaA] [Campylobacter lari]	412	e-114
<input type="checkbox"/>	tr	Q8VN90	Flagellin A (Fragment) [flaA] [Helicobacter pylori (Ca...]	383	e-105
<input type="checkbox"/>	tr	Q8VN91	Flagellin A (Fragment) [flaA] [Helicobacter pylori (Ca...]	382	e-105
<input type="checkbox"/>	tr	Q8VLN3	Flagellin A (Fragment) [flaA] [Helicobacter pylori (Ca...]	382	e-105
<input type="checkbox"/>	sp	Q07910	FLAB_HELMU Flagellin B (Flagellin N) [flaB] [Helicobac...]	381	e-104
<input type="checkbox"/>	tr	Q7X2D0	Flagellin B [flaB] [Helicobacter pylori (Campylobacter...]	380	e-104
<input type="checkbox"/>	tr	Q8RNU8	Flagellin B subunit [flaB] [Helicobacter pylori (Campy...]	378	e-103
<input type="checkbox"/>	sp	Q07911	FLAB_HELPY Flagellin B (Flagellin N) [flaB] [Helicobac...]	377	e-103
<input type="checkbox"/>	sp	Q9ZMV8	FLAB_HELPJ Flagellin B (Flagellin N) [flaB] [Helicobac...]	377	e-103
<input type="checkbox"/>	tr	Q6VYQ1	Flagellin B [flaB] [Helicobacter pylori (Campylobacter...]	377	e-103
<input type="checkbox"/>	tr	Q9XB37	Flagellin B [flaB] [Helicobacter felis]	373	e-102
<input type="checkbox"/>	tr	Q7TTM9	Major flagellin subunit FlaA_1 (Major flagellin subuni...]	368	e-100
<input type="checkbox"/>	tr	Q7VF81	Minor flagellin subunit FlaB [flaB] [Helicobacter hepa...]	357	4e-97
<input type="checkbox"/>	sp	P50612	FLAA_HELMU Flagellin A [flaA] [Helicobacter mustelae]	345	1e-93
<input type="checkbox"/>	tr	Q93NM1	Flagellin A (Fragment) [flaA] [Campylobacter jejuni]	337	4e-91
<input type="checkbox"/>	tr	Q93NM0	Flagellin A (Fragment) [flaA] [Campylobacter jejuni]	337	4e-91
<input type="checkbox"/>	tr	Q8VN93	Flagellin B (Fragment) [flaB] [Helicobacter pylori (Ca...]	337	5e-91

Graphical overview of the alignments

[Click here](#)

to resubmit your query after masking regions matching PROSITE profiles or Pfam HMMs

([?](#) Help) (use ScanProsite for more details about PROSITE matches)

Profile hits

Pfam hits

Flagellin_N

Flagell

Flagel

Flagelli

Submission	Matches on query sequence		Mat
	1	500	
FLA2_CAMJE			
085179			
Q9R950			
Q9R953			
Q9RF26			
085183			
Q8G9F3			
Q7X516			
Q9RF25			
FLB2_CAMJE			
Q9RPY6			
Q99Q27			
Q99QL6			
Q93NL6			
Q93NL9			
FLAA_CAMCO			
Q841B9			
Q46009			
FLAB_CAMCO			
FLA3_CAMJE			
Q841B8			
Q9R952			
FLA1_CAMJE			
085182			
Q9R949			
Q30696			
Q30689			
Q8G9F2			
Q34938			
085180			
Q8G9F1			
FLB3_CAMJE			
Q8G9F0			
Q79AR6			
FLB1_CAMJE			
Q6L5K6			
Q6L5J8			
Q9R951			
Q933V4			
Q6L5K1			
Q9R954			
Q6L5J9			
Q93NL8			
Q93NL7			
Q6L5K5			
Q6L5K8			
Q6L5J7			
Q6L5K2			
Q6L5K9			
Q6L5L0			
Q6L5K4			
Q6L5K7			
Q6L5J6			
Q6L5L1			
085181			
Q6L5K0			
Q6L5K3			
P96751			
P96752			
Q84IC4			
Q84IC5			
Q84IC7			
Q84IC8			
Q93GT4			
Q8RTY4			
Q56746			
Q93R24			
Q7H7N1			
Q84IC9			
Q93GT1			
Q84IC3			
Q84IC6			
Q84IC2			
Q93GT2			
Q84IC1			
Q93GT3			
Q46462			
Q46461			
FLAA_HELFE			
Q7X2D1			
FLAA_HELPY			
Q8GD49			
Q6VYQ2			
Q84IC0			
Q8VN98			
Q8VN91			

Alignments

sp P22251 **Flagellin A [flaA] [Campylobacter jejuni]** 575 AA
FLA2_CAMJE align

Score = 983 bits (2542), Expect = 0.0
Identities = 526/575 (91%), Positives = 526/575 (91%)

Query: 1 GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 1 GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60

Query: 61 GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME
Sbjct: 61 GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120

Query: 121 ELDNIAINTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
ELDNIAINTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF
Sbjct: 121 ELDNIAINTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180

Query: 181 TSGVVGLTIKNGYNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVRATYDVKTGTG 240
TSGVVGLTIKNGYNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVRATYDVKTGTG
Sbjct: 181 TSGVVGLTIKNGYNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVRATYDVKTGTG 240

Query: 241 YAIKEGTTSDFAINGVTIGKIEYKDGDNGLISAINAVKDTTGVQASKDENGKLVLT 300
YAIKEGTTSDFAINGVTIGKIEYKDGDNGLISAINAVKDTTGVQASKDENGKLVLT
Sbjct: 241 YAIKEGTTSDFAINGVTIGKIEYKDGDNGLISAINAVKDTTGVQASKDENGKLVLT 300

Query: 301 ADGRGIKITGDIGVSGILANQKENYGRSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
ADGRGIKITGDIGVSGILANQKENYGRSLVKNDGRDINISGTNLSAIGMGTTDMISQS
Sbjct: 301 ADGRGIKITGDIGVSGILANQKENYGRSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360

Query: 361 SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXXXX 420
SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFM
Sbjct: 361 SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMSAQSGFSRGSFSGSVGS 420

Query: 421 XKNLXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXXXXQFAALKTTAANTTDETAGVT 480
KNL NTYVV QFAALKTTAANTTDETAGVT
Sbjct: 421 GKNLSVGLSQGIQIISAA SMSNTYVVSAGSGFSSGSGNSQFAALKTTAANTTDETAGVT 480

Query: 481 TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 540
TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA
Sbjct: 481 TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 540

Query: 541 SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ
Sbjct: 541 SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575

tr O85179 **Flagellin A [flaA] [Campylobacter jejuni]** 576 AA
align

Score = 983 bits (2542), Expect = 0.0
Identities = 526/575 (91%), Positives = 526/575 (91%)

```

Query: 1   GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
          GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 2   GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 61

Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
          GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME
Sbjct: 62  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 121

Query: 121 ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
          ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF
Sbjct: 122 ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 181

Query: 181 TSGVVGLTIKNGYNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVRATYDVKTTGV 240
          TSGVVGLTIKNGYNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVRATYDVKTTGV
Sbjct: 182 TSGVVGLTIKNGYNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVRATYDVKTTGV 241

Query: 241 YAIKEGTTSDFAINGVTIGKIEYKDGDNGLSLISAINAVKDTTGVQASKDENGKLVLT 300
          YAIKEGTTSDFAINGVTIGKIEYKDGDNGLSLISAINAVKDTTGVQASKDENGKLVLT
Sbjct: 242 YAIKEGTTSDFAINGVTIGKIEYKDGDNGLSLISAINAVKDTTGVQASKDENGKLVLT 301

Query: 301 ADGRGIKITGDIGVSGILANQKENYGRSLVKN DGRDINISGTNLSAIGMGTTDMISQS 360
          ADGRGIKITGDIGVSGILANQKENYGRSLVKN DGRDINISGTNLSAIGMGTTDMISQS
Sbjct: 302 ADGRGIKITGDIGVSGILANQKENYGRSLVKN DGRDINISGTNLSAIGMGTTDMISQS 361

Query: 361 SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXXXX 420
          SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFM
Sbjct: 362 SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMSAQDSGFSRSGFSVGS 421

Query: 421 XKNLXXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXXXQFAALKTTAANTTDETAGVT 480
          KNL                      NTYVV                      QFAALKTTAANTTDETAGVT
Sbjct: 422 GKNLSVGLSQGIQIISAA SMSNTYVVSAGSGFSSGSGNSQFAALKTTAANTTDETAGVT 481

Query: 481 TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 540
          TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA
Sbjct: 482 TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 541

Query: 541 SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
          SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ
Sbjct: 542 SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 576

```

```

tr      Q9R950      Flagellin A [flaA] [Campylobacter jejuni]      576 AA
                                align

```

Score = 979 bits (2532), Expect = 0.0
Identities = 524/575 (91%), Positives = 526/575 (91%)

```

Query: 1   GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
          GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 2   GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 61

Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
          GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME
Sbjct: 62  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 121

Query: 121 ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180

```

```

ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF
Sbjct: 122 ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 181

Query: 181 TSGVVGLTIKNGIEDFKFDNVVISTSVGTGLGALAEIINKSADKTGVRATYDVKTTGV 240
TSGVVGLTIKNGIEDFKFDNVVISTSVGTGLGALAEIINKSADKTGVRATYDVKTTGV
Sbjct: 182 TSGVVGLTIKNGIEDFKFDNVVISTSVGTGLGALAEIINKSADKTGVRATYDVKTTGV 241

Query: 241 YAIKEGTTSDFAINGVTIGKIEYKDGNGSLISAINAVKDTTGVQASKDENGKLVLT 300
YAIKEGTTSQ+FAINGVTIGKIEYKDGNGSLISAINAVKDTTGVQASKDENGKLVLT
Sbjct: 242 YAIKEGTTSQNFAINGVTIGKIEYKDGNGSLISAINAVKDTTGVQASKDENGKLVLT 301

Query: 301 ADGRGIKITGDIGVSGILANQKENYGRSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
ADGRGIKITGDIGVSGILANQKENYGRSLVKNDGRDINISGTNLSAIGMGTTDMISQS
Sbjct: 302 ADGRGIKITGDIGVSGILANQKENYGRSLVKNDGRDINISGTNLSAIGMGTTDMISQS 361

Query: 361 SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXX 420
SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFM
Sbjct: 362 SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMSAQSGFSRGSGFSVGS 421

Query: 421 XKNLXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXXXQFAALKTTAANTTDETAGVT 480
KNL NTYVV QFAALKTTAANTTDETAGVT
Sbjct: 422 GKNLSVGLSQGIQIISSAASMSNTYVVSAGSGFSSGSGNSQFAALKTTAANTTDETAGVT 481

Query: 481 TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 540
TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA
Sbjct: 482 TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 541

Query: 541 SESANYSKANILAQSGSYAMAAQANSSQQNVLRLLQ 575
SESANYSKANILAQSGS+AMAAQANSSQQNVLRLLQ
Sbjct: 542 SESANYSKANILAQSGSHAMAAQANSSQQNVLRLLQ 576

```

tr Q9R953 **Flagellin A [flaA] [Campylobacter jejuni]** 576 AA align

Score = 979 bits (2530), Expect = 0.0
Identities = 524/575 (91%), Positives = 525/575 (91%)

```

Query: 1 GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
GFRINTN AALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 2 GFRINTNGAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 61

Query: 61 GQAI SNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
GQAI SNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME
Sbjct: 62 GQAI SNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 121

Query: 121 ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF
Sbjct: 122 ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 181

Query: 181 TSGVVGLTIKNGIEDFKFDNVVISTSVGTGLGALAEIINKSADKTGVRATYDVKTTGV 240
TSGVVGLTIKNGIEDFKFDNVVISTSVGTGLGALAEIINKSADKTGVRATYDVKTTGV
Sbjct: 182 TSGVVGLTIKNGIEDFKFDNVVISTSVGTGLGALAEIINKSADKTGVRATYDVKTTGV 241

Query: 241 YAIKEGTTSDFAINGVTIGKIEYKDGNGSLISAINAVKDTTGVQASKDENGKLVLT 300
YAIKEGTTSQ+FAINGVTIGKIEYKDGNGSLISAINAVKDTTGVQASKDENGKLVLT

```

Sbjct: 242 YAIKEGTTSQEFAINGVTIGKIEYKDGNGSLISAINAVKDTTGVQASKDENGKLVLT 301

Query: 301 ADGRGIKITGDIGVSGILANQKENYGRSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
ADGRGIKITGDIGVSGILANQKENYGRSLVKNDGRDINISGTNLSAIGMGTTDMISQS

Sbjct: 302 ADGRGIKITGDIGVSGILANQKENYGRSLVKNDGRDINISGTNLSAIGMGTTDMISQS 361

Query: 361 SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXX 420
SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFM

Sbjct: 362 SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMSAQSGFSRSGGFSVGS 421

Query: 421 KKNLXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXXXQFAALKTTAANTTDETAGVT 480
KNL NTYVV QFAALKTTAANTTDETAGVT

Sbjct: 422 GKNLSVGLSQGIQIISAGSMSNTYVVSAGSGFSSGSGNSQFAALKTTAANTTDETAGVT 481

Query: 481 TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 540
TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA

Sbjct: 482 TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 541

Query: 541 SESANYSKANILAQSGSYAMAQANSSQQNVRLRLQ 575
SESANYSKANILAQSGSYAMAQANSSQQNVRLRLQ

Sbjct: 542 SESANYSKANILAQSGSYAMAQANSSQQNVRLRLQ 576

tr Q9RF26 Chimeric flagellin A/B [*Campylobacter jejuni*] 576 AA
align

Score = 977 bits (2526), Expect = 0.0
Identities = 522/575 (90%), Positives = 525/575 (90%)

Query: 1 GFRINTNVAALNAKANSDLNAKSLDASLRLSSGLRINSAADDASGMAIADSLRSQANTL 60
GFRINTNVAALNAKANSDLNAKSLDASLRLSSGLRINSAADDASGMAIADSLRSQA TL

Sbjct: 2 GFRINTNVAALNAKANSDLNAKSLDASLRLSSGLRINSAADDASGMAIADSLRSQAATL 61

Query: 61 GQAI+NGNDA+GILQTADKAMDEQLKILDITIKTKATQAAQDGQSLKTRTMLQADINKLME 120
GQAI+NGNDA+GILQTADKAMDEQLKILDITIKTKATQAAQDGQSLKTRTMLQADIN+LME

Sbjct: 62 GQAINNGNDAIGILQTADKAMDEQLKILDITIKTKATQAAQDGQSLKTRTMLQADINRLME 121

Query: 121 ELDNIANTTSPFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
ELDNIANTTSPFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF

Sbjct: 122 ELDNIANTTSPFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 181

Query: 181 TSGVVGLTIKNGIEDFKFDNVVISTSVGTGLGALAEIINKSADKTGVRATYDVKTGTV 240
TSGVVGLTIKNGIEDFKFDNVVISTSVGTGLGALAEIINKSADKTGVRATYDVKTGTV

Sbjct: 182 TSGVVGLTIKNGIEDFKFDNVVISTSVGTGLGALAEIINKSADKTGVRATYDVKTGTV 241

Query: 241 YAIKEGTTSQDFAINGVTIGKIEYKDGNGSLISAINAVKDTTGVQASKDENGKLVLT 300
YAIKEGTTSQDFAINGVTIGKIEYKDGNGSLISAINAVKDTTGVQASKDENGKLVLT

Sbjct: 242 YAIKEGTTSQDFAINGVTIGKIEYKDGNGSLISAINAVKDTTGVQASKDENGKLVLT 301

Query: 301 ADGRGIKITGDIGVSGILANQKENYGRSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
ADGRGIKITGDIGVSGILANQKENYGRSLVKNDGRDINISGTNLSAIGMGTTDMISQS

Sbjct: 302 ADGRGIKITGDIGVSGILANQKENYGRSLVKNDGRDINISGTNLSAIGMGTTDMISQS 361

Query: 361 SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXX 420
SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFM

Sbjct: 362 SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMSAQSGFSRSGGFSVGS 421

```
Query: 421 XKNLXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXQFAALKTTAANTTDETAGVT 480
          KNL                      NTYVV                      QFAALKTTAANTTDETAGVT
Sbjct: 422 GKNLSVGLSQGIQIISAAASMSNTYVVSAGSGFSSGSGNSQFAALKTTAANTTDETAGVT 481

Query: 481 TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 540
          TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA
Sbjct: 482 TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 541

Query: 541 SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
          SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ
Sbjct: 542 SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 576
```

```
tr      085183      Flagellin A [flaA] [Campylobacter jejuni]      576 AA
                                align
```

Score = 957 bits (2475), Expect = 0.0
Identities = 509/575 (88%), Positives = 517/575 (89%)

```
Query: 1   GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
          GFRINTNV+ALNAK NSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQ NTL
Sbjct: 2   GFRINTNVSAALNAKPNSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQTNTL 61

Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDITIKTKATQAAQDGQSLKTRTMLQADINKLME 120
          GQAISNGNDALGILQTADKAMDEQLKILDITIKTKATQAAQDGQSLKTRTMLQADIN+LME
Sbjct: 62  GQAISNGNDALGILQTADKAMDEQLKILDITIKTKATQAAQDGQSLKTRTMLQADINRLME 121

Query: 121 ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
          ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF
Sbjct: 122 ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 181

Query: 181 TSGVVGLTIKNGYNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVRATYDVKTTGV 240
          TSGVVGLTIKNGYNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVRATYDVKTTGV
Sbjct: 182 TSGVVGLTIKNGYNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVRATYDVKTTGV 241

Query: 241 YAIKEGTTTSQDFAINGVTIGKIEYKDGNGSLISAINAVKDTTGVQASKDENGKLVLT 300
          YAIKEGTTTSQ+FAINGV IG+I YKGDG NG L+SAINAVKDTTGVQASKDENGKLVLT
Sbjct: 242 YAIKEGTTTSQNFINGVVIGQINYKGDGNNQGLVSAINAVKDTTGVQASKDENGKLVLT 301

Query: 301 ADGRGIKITGDIGVSGGILANQKENYGRSLVKNDGRDINISGTNLSAIGMGTDDMISQS 360
          ADGRGIKITGDIGVSGGILANQKENYGRSLVKNDGRDINISGTNLSAIGMGTDDMISQS
Sbjct: 302 ADGRGIKITGDIGVSGGILANQKENYGRSLVKNDGRDINISGTNLSAIGMGTDDMISQS 361

Query: 361 SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXXXX 420
          SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFM
Sbjct: 362 SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMSAQSGFSRSGSGFSVGS 421

Query: 421 XKNLXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXQFAALKTTAANTTDETAGVT 480
          KNL                      NTYVV                      QF  LKTTAANTTDETAGVT
Sbjct: 422 GKNLSVGLSQGIQIISAAASMSNTYVVSAGSGFSSGSGNSQFGVLKTTAANTTDETAGVT 481

Query: 481 TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 540
          TLKGAMA MDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDF+
Sbjct: 482 TLKGAMAGMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFS 541
```


Query: 541 SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
 SESANYSKANILAQSGSY+MAQANSSQQNVLRLLQ
 Sbjct: 542 SESANYSKANILAQSGSYMAQANSSQQNVLRLLQ 576

tr Q8G9F3 **Flagellin (Fragment) [flaA] [Campylobacter coli]** 575 AA
align

Score = 956 bits (2471), Expect = 0.0
 Identities = 511/575 (88%), Positives = 519/575 (89%)

Query: 1 GFRINTNVAALNAKANSDLNAKSLDASLRLSSGLRINSAADDASGMAIADSLRSQANTL 60
 GFRINTN AALNAKANSDLN+KSLD SL+RLSSGLRINSAADDASGMAIADSLRSQA+TL
 Sbjct: 1 GFRINTNGAALNAKANSDLNSKSLDQSLARLSSGLRINSAADDASGMAIADSLRSQASTL 60

Query: 61 GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
 GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LME
 Sbjct: 61 GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120

Query: 121 ELDNIAINTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
 ELDNIAINTTSFNGKQLLSG FTNQEFQIGASSNQ+KATIGATQSSKIGVTRFETGAQSF
 Sbjct: 121 ELDNIAINTTSFNGKQLLSGGFTNQEFQIGASSNQTIKATIGATQSSKIGVTRFETGAQSF 180

Query: 181 TSGVVGLTIKNGYNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVRATYDVKTGTGV 240
 TSGVVGLTIKNGYNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVRATYDVKTGTGV
 Sbjct: 181 TSGVVGLTIKNGYNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVRATYDVKTGTGV 240

Query: 241 YAIKEGTTSDFAINGVTIGKIEYKDGNGSLISAINAVKDTTGVQASKDENGKLVLT 300
 YAIKEGTTSDFAINGVTIGKIEYKDGNG+GSLISAINAVKDTTGVQASKDENGKLVLT
 Sbjct: 241 YAIKEGTTSDFAINGVTIGKIEYKDGNGDGLISAINAVKDTTGVQASKDENGKLVLT 300

Query: 301 ADGRGIKITGDIGVSGILANQKENYGRSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
 ADGRGIKITGDIGVSGILANQKENYGRSLVKNDGRDINISGTNLSAIGMGTTDMISQS
 Sbjct: 301 ADGRGIKITGDIGVSGILANQKENYGRSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360

Query: 361 SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXX 420
 SVSLRESKGQISATNADAMGFNSYKGGGK V + VSSISAFM
 Sbjct: 361 SVSLRESKGQISATNADAMGFNSYKGGGKLVLSAVSSISAFMSAQN SGFSRSGFSVGS 420

Query: 421 XKNLXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXXXQFAALKTTAANTTDETAGVT 480
 KNL NTYVV QFAALKTTAANTTDETAGVT
 Sbjct: 421 GKNLSVGLNQGIQIISAA SMSNTYVVSAGSGFSSGSGNSQFAALKTTAANTTDETAGVT 480

Query: 481 TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 540
 TLKGAMAVMD+AETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA
 Sbjct: 481 TLKGAMAVMDMAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 540

Query: 541 SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
 SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ
 Sbjct: 541 SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575

tr Q7X516 **FlaB [flaB] [Campylobacter jejuni]** 576 AA
align

Score = 935 bits (2417), Expect = 0.0
Identities = 497/575 (86%), Positives = 510/575 (88%)

```

Query: 1   GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
          GFRINTN+ ALNA ANS +N+ LD SLSRLSSGLRINSAADDASGMAIADSLRSQA TL
Sbjct: 2   GFRINTNIGALNAHANSVVNSNELDKSLRLSSGLRINSAADDASGMAIADSLRSQAATL 61

Query: 61  GQAIISNGNDALGILQTADKAMDEQLKILDITIKTKATQAAQDGQSLKTRTMLQADINKLME 120
          GQAI+NGNDA+GILQTADKAMDEQLKILDITIKTKATQAAQDGQSLKTRTMLQADINKLME
Sbjct: 62  GQAINNGNDAIGILQTADKAMDEQLKILDITIKTKATQAAQDGQSLKTRTMLQADINKLME 121

Query: 121  ELDNIANTTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
          ELDNIANTTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF
Sbjct: 122  ELDNIANTTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 181

Query: 181  TSGVVGLTIKNGYNGIEDFKFDNVVISTSVGTGLGALAEIINKSADKTGVRATYDVKTTGV 240
          TSGVVGLTIKNGYNGIEDFKFDNVVISTSVGTGLGALAEIINKSADKTGVRATYDVKTTGV
Sbjct: 182  TSGVVGLTIKNGYNGIEDFKFDNVVISTSVGTGLGALAEIINKSADKTGVRATYDVKTTGV 241

Query: 241  YAIKEGTTSDFAINGVTIGKIEYKDGNGSLISAINAVKDTTGVQASKDENGKLV LTS 300
          YAIKEGTTSDFAINGV IG+I YKGDG NG L+SAINAVKDTTGVQASKDENGKLV LTS
Sbjct: 242  YAIKEGTTSDFAINGVAIGQINYKGDGNNQGLVSAINAVKDTTGVQASKDENGKLV LTS 301

Query: 301  ADGRGIKITGDIGVGSGILANQKENYGRSLSVKNDGRDINISGTNLSAIGMGTTDMISQS 360
          ADGRGIKITGDIGVGSGILANQKENYGRSLSVKNDGRDINISGTNLSAIGMGTTDMISQS
Sbjct: 302  ADGRGIKITGDIGVGSGILANQKENYGRSLSVKNDGRDINISGTNLSAIGMGTTDMISQS 361

Query: 361  SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXXXX 420
          SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFM
Sbjct: 362  SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMSAQSGFSRSGSFGSVGS 421

Query: 421  XKNLXXXXXXXXXXXXXXXXXXXXNTYVXXXXXXXXXXXXXXXXXQFAALKTTAANTTDETAGVT 480
          KNL NTYVV QFAALKTTAANTTDETAGVT
Sbjct: 422  GKNLSVGLSQGIQIISAAASMSNTYVVSAGSGFSSGSGNSQFAALKTTAANTTDETAGVT 481

Query: 481  TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 540
          TLKGAMAVMDIAETAITNLDQIRADIGS+QNN+ TINNITVTQVNVKAAES IRDVDFA
Sbjct: 482  TLKGAMAVMDIAETAITNLDQIRADIGSVQNQLQVTINNITVTQVNVKAAESTIRDVDFA 541

Query: 541  SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
          SESAN+SK NILAQSGSYAM+QAN+ QQNVL+LLQ
Sbjct: 542  SESANFSKYNILAQSGSYAMSQANAVQQNVLKLQ 576

```

tr Q9RF25 **Flagellin B [flaB] [Campylobacter jejuni]** 576 AA
align

Score = 934 bits (2413), Expect = 0.0
Identities = 495/575 (86%), Positives = 510/575 (88%)

```

Query: 1   GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
          GFRINTN+ ALNA ANS +N+ LD SLSRLSSGLRINSAADDASGMAIADSLRSQA TL
Sbjct: 2   GFRINTNIGALNAHANSVVNSNELDKSLRLSSGLRINSAADDASGMAIADSLRSQAATL 61

Query: 61  GQAIISNGNDALGILQTADKAMDEQLKILDITIKTKATQAAQDGQSLKTRTMLQADINKLME 120
          GQAI+NGNDA+GILQTADKAMDEQLKILDITIKTKATQAAQDGQSLKTRTMLQADIN+LME

```

```

Sbjct: 62  GQAINNGNDAIGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 121

Query: 121  ELDNIANTTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
           ELDNIANTTTSFNGKQLLSGNFTNQEFQIGASSNQ+KATIGATQSSKIGVTRFETGAQSF
Sbjct: 122  ELDNIANTTTSFNGKQLLSGNFTNQEFQIGASSNQTIKATIGATQSSKIGVTRFETGAQSF 181

Query: 181  TSGVVGLTIKNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVRATYDVKTTGV 240
           TSGVVGLTIKNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVRATYDVKTTGV
Sbjct: 182  TSGVVGLTIKNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVRATYDVKTTGV 241

Query: 241  YAIKEGTTSDFAINGVTIGKIEYKDGNGSLISAINAVKDTTGVQASKDENGKLVLT 300
           YAIKEGTTSDFAINGV IG+I YKGDG NG L+SAINAVKDTTGVQASKDENGKLVLT
Sbjct: 242  YAIKEGTTSDFAINGVVIGQINYKGDNGQLVSAINAVKDTTGVQASKDENGKLVLT 301

Query: 301  ADGRGIKITGDIGVSGILANQKENYGRSLVKNDGRDINISG'TNLSAIGMGT'TDMISQS 360
           ADGRGIKITGDIGVSGILANQKENYGRSLVKNDGRDINISG'TNLSAIGMGT'TDMISQS
Sbjct: 302  ADGRGIKITGDIGVSGILANQKENYGRSLVKNDGRDINISG'TNLSAIGMGT'TDMISQS 361

Query: 361  SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXXXX 420
           SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFM
Sbjct: 362  SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMSAQSGFSRSGFSVGS 421

Query: 421  XKNLXXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXQFAALKTTAANTTDETAGVT 480
           KNL NTYVV QFAALKTTAANTTDETAGVT
Sbjct: 422  GKNLSVGLSQGIQIISSAASMSNTYVVSAGSGFSSGSGNSQFAALKTTAANTTDETAGVT 481

Query: 481  TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 540
           TLKGAMAVMDIAETAITNLDQIRADIGS+QNQ+ TINNITVTQVNVKAAES IRDVDFA
Sbjct: 482  TLKGAMAVMDIAETAITNLDQIRADIGSVQNQLQVTINNITVTQVNVKAAESTIRDVDFA 541

Query: 541  SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
           SESAN+SK NILAQSGSYAM+QAN+ QQNVL+LLQ
Sbjct: 542  SESANFSKYNILAQSGSYAMSQANAVQQNVLKLLQ 576

```

```

sp      P22252      Flagellin B [flaB] [Campylobacter jejuni] 575 AA
       FLB2_CAMJE      align

```

Score = 932 bits (2408), Expect = 0.0
Identities = 494/575 (85%), Positives = 509/575 (87%)

```

Query: 1  GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
           GFRINTN+ ALNA ANS +N+ LD SLSRLSSGLRINSAADDASGMAIADSLRSQA TL
Sbjct: 1  GFRINTNIGALNAHANSVVSNSELDKSLRLSSGLRINSAADDASGMAIADSLRSQAATL 60

Query: 61  GQAINNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
           GQAI+NGNDA+GILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LME
Sbjct: 61  GQAINNGNDAIGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120

Query: 121  ELDNIANTTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
           ELDNIANTTTSFNGKQLLSGNFTNQEFQIGASSNQ+KATIGATQSSKIGVTRFETGAQSF
Sbjct: 121  ELDNIANTTTSFNGKQLLSGNFTNQEFQIGASSNQTIKATIGATQSSKIGVTRFETGAQSF 180

Query: 181  TSGVVGLTIKNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVRATYDVKTTGV 240
           TSGVVGLTIKNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVRATYDVKTTGV
Sbjct: 181  TSGVVGLTIKNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVRATYDVKTTGV 240

```

```

Query: 241 YAIKEGTTSDFAINGVTIGKIEYKDGNGSLISAINAVKDTTGVQASKDENGKLVLT 300
          YAIKEGTTSDFAINGV IG+I YKGDG NG L+SAINAVKDTTGVQASKDENGKLVLT
Sbjct: 241 YAIKEGTTSDFAINGVVIGQINIKDGDNGQLVSAINAVKDTTGVQASKDENGKLVLT 300

Query: 301 ADGRGIKITGDIGVSGILANQKENYGRSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
          ADGRGIKITGDIGVSGILANQKENYGRSLVKNDGRDINISGTNLSAIGMGTTDMISQS
Sbjct: 301 ADGRGIKITGDIGVSGILANQKENYGRSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360

Query: 361 SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXX 420
          SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFM
Sbjct: 361 SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMSAQSGFSRGSFSGSVGS 420

Query: 421 XKNLXXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXQFAALKTTAANTTDETAGVT 480
          KNL                      NTYVV                      QFAALKTTAANTTDETAGVT
Sbjct: 421 GKNLSVGLSQGIQIISAA SMSNTYVVSAGSGFSSGSGNSQFAALKTTAANTTDETAGVT 480

Query: 481 TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 540
          TLKGAMAVMDIAETAITNLDQIRADIGS+QNQ+ TINNITVTQVNVKAAES IRDVDFA
Sbjct: 481 TLKGAMAVMDIAETAITNLDQIRADIGSVQNQLQVTINNITVTQVNVKAAESTIRDVDFA 540

Query: 541 SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
          SESAN+SK NILAQSGSYAM+Q N+ QQNVL+LLQ
Sbjct: 541 SESANFSKYNILAQSGSYAMSQRNAVQQNVLRLLQ 575

```

tr Q9RPY6 **Flagellin A [flaA] [Campylobacter jejuni]** 574 AA
align

Score = 918 bits (2372), Expect = 0.0
Identities = 489/575 (85%), Positives = 506/575 (87%), Gaps = 2/575 (0%)

```

Query: 1    GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
          GFRINTNVAALNAKANSDLN+++LD SLSRLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 2    GFRINTNVAALNAKANSDLNSRALDQSLRLSSGLRINSAADDASGMAIADSLRSQANTL 61

Query: 61    GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
          GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LME
Sbjct: 62    GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 121

Query: 121    ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
          ELDNIANTTSFNGKQLLSG FTNQEFQIG+SSNQ+KA+IGATQSSKIGVTRFETG+QSF
Sbjct: 122    ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 181

Query: 181    TSGVVGLTIKKNYNGIEDFKFDNVVISTSVGTGLGALAEIEINKSADKTGVRATYDVKTGGV 240
          +SG VGLTIKKNYNGIEDFKFD+VVISTSVGTGLGALAEIEIN++ADKTG+RAT+DVK+ G
Sbjct: 182    SSGTVGLTIKKNYNGIEDFKFDSVVISTSVGTGLGALAEIEINRNADKTGIRATFDVKS VGA 241

Query: 241    YAIKEGTTSDFAINGVTIGKIEYKDGNGSLISAINAVKDTTGVQASKDENGKLVLT 300
          YAIK G TSQDFAINGV IG+I Y DGD NG LISAINAVKDTTGVQASKDENGKLVLT
Sbjct: 242    YAIKAGNTS QDFAINGVVIGQINYN DGDNGQLISAINAVKDTTGVQASKDENGKLVLT 301

Query: 301    ADGRGIKITGDIGVSGILANQKENYGRSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
          ADGRGIKITG IGVG+GIL    ENYGRSLVKNDGRDINISGT LSAIMG TDMISQS
Sbjct: 302    ADGRGIKITGSIGVGAGIL--HTENYGRSLVKNDGRDINISGTGLSAIMGATDMISQS 359

```

Query: 361 SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXX 420
SVSLRESKGQISA NADAMGFNSYKGGGKFVFTQNVSSISAFM
Sbjct: 360 SVSLRESKGQISANADAMGFNSYKGGGKFVFTQNVSSISAFMSAQSGFSRGSFSGFSVGS 419

Query: 421 XKNLXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXQFAALKTTAANTTDETAGVT 480
KNL NTYVV QFAALKTTAANTTDETAGVT
Sbjct: 420 GKNLSVGLSQGIQIISSAASMSNTYVVSAGSGFSSGSGNSQFAALKTTAANTTDETAGVT 479

Query: 481 TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 540
TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA
Sbjct: 480 TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 539

Query: 541 SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ
Sbjct: 540 SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 574

tr Q99Q27 **Flagellin A (Fragment) [flaA] [Campylobacter jejuni]** 576 AA
align

Score = 905 bits (2340), Expect = 0.0

Identities = 484/576 (84%), Positives = 501/576 (86%), Gaps = 1/576 (0%)

Query: 1 GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
GFRINTN AALNAKANSDLNAKSLD+SL+RLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 1 GFRINTNGAALNAKANSDLNAKSLDSSLARLSSGLRINSAADDASGMAIADSLRSQANTL 60

Query: 61 GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME
Sbjct: 61 GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120

Query: 121 ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
ELDNIANTTSFNGKQLLSG FTNQEFQIG+SSNQTVKATIGATQSSKIGVTRFETG+QSF
Sbjct: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTVKATIGATQSSKIGVTRFETGSQSF 180

Query: 181 TSGVVGLTIKKNYNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVRATYDVKTTGV 240
TSGVVGLTIKKNYNGIEDFKFDNVVISTSVGTGLGALAEINK+ADKTGVRATYDVKTTG
Sbjct: 181 TSGVVGLTIKKNYNGIEDFKFDNVVISTSVGTGLGALAEINKNADKTGVRATYDVKTTGA 240

Query: 241 YAIKEGTTSDFAINGVTIGKIEYKDGNGSLISAINAVKDTTGVQASKDENGKLVLT 300
YAIK GTTSQDFAINGV IGK++YKGDG NGSLISAINAVKDTTGVQASKDENGKLVLT
Sbjct: 241 YAIKAGTTSDFAINGVIIKVDYKGDNNGSLISAINAVKDTTGVQASKDENGKLVLT 300

Query: 301 ADGRGIKITGDIGVSGILANQKENYGRSLVKN DGRDINISGTNLSAIGMGTTDMISQS 360
ADGRGIKITGDIGVSGIL+ QKENYGRSLVKN DGRDIN+SGT LSAIMG DMISQ+
Sbjct: 301 ADGRGIKITGDIGVSGILSAQKENYGRSLVKN DGRDINVSGTGLSAIGMGADMISQA 360

Query: 361 SVSLRESKGQISATNADAMGFNSYKGGG-KFVFTQNVSSISAFMXXXXXXXXXXXXXXXXX 419
SVSLRESKGQISA NADAMGFNSY GGG K + SSISAFM
Sbjct: 361 SVSLRESKGQISANADAMGFNSYNGGAKQILQVQASSISAFMSQAGSGFSAGSGFSAG 420

Query: 420 XXKNLXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXQFAALKTTAANTTDETAGV 479
K +TYV+ QFAALKT+ + + TAGV
Sbjct: 421 SGKGYSTILSGSVQIVSSTASMSSTYVISAGSGFSVGSGNSQFAALKTSTVSAHEATAGV 480

Query: 480 TTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDF 539

TTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVK+AESQIRDVDF
Sbjct: 481 TTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKSAESQIRDVDF 540

Query: 540 ASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
ASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ

Sbjct: 541 ASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 576

tr Q99QL6 Flagellin A (Fragment) [flaA] [Campylobacter jejuni] 574 AA
align

Score = 905 bits (2338), Expect = 0.0

Identities = 484/575 (84%), Positives = 500/575 (86%), Gaps = 1/575 (0%)

Query: 1 GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
GFRINTN AALNAKANSDLNAKSLD+SL+RLSSGLRINSAADDASGMAIADSLRSQANTL

Sbjct: 1 GFRINTNGAALNAKANSDLNAKSLDSSLARLSSGLRINSAADDASGMAIADSLRSQANTL 60

Query: 61 GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME

Sbjct: 61 GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120

Query: 121 ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
ELDNIANTTSFNGKQLLSG FTNQEFQIG+SSNQTVKATIGATQSSKIGVTRFETG+QSF

Sbjct: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTVKATIGATQSSKIGVTRFETGSQSF 180

Query: 181 TSGVVGLTIKNGYIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVRATYDVKTGTV 240
TSGVVGLTIKNGYIEDFKFDNVVISTSVGTGLGALAEINK+ADKTGVRATYDVKTGTV

Sbjct: 181 TSGVVGLTIKNGYIEDFKFDNVVISTSVGTGLGALAEINKNADKTGVRATYDVKTGTV 240

Query: 241 YAIKEGTTSDFAINGVTIGKIEYKDGNGSLISAINAVKDTTGVQASKDENGKLVLT 300
YAIK GTTSDFAINGV IGK++YKGDG NGSLISAINAVKDTTGVQASKDENGKLVLT

Sbjct: 241 YAIKAGTTSDFAINGVIIGKVDYKGDGNGSLISAINAVKDTTGVQASKDENGKLVLT 300

Query: 301 ADGRGIKITGDIGVSGGILANQKENYGRSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
ADGRGIKITGDIGVSGGIL+ QKENYGRSLVKNDGRDIN+SGT LSAIGMG DMISQ+

Sbjct: 301 ADGRGIKITGDIGVSGGILSTQKENYGRSLVKNDGRDINVSGTGLSAIGMGAAADMISQA 360

Query: 361 SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXX 420
SVSLRESKGQISA NADAMGFNSY GGG Q SSISAFM

Sbjct: 361 SVSLRESKGQISANADAMGFNSYNGGAKQILQ-ASSISAFMSQAGSGFSAGSGFSAGS 419

Query: 421 XKNLXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXXXQFAALKTTAANTTDETAGVT 480
K +TYV+ QFAALKT+ + + TAGVT

Sbjct: 420 GKGYSTILSGSVQIVSSTASMSSTYVISEGSGFSAGSGNSQFAALKTTSTVSAHEATAGVT 479

Query: 481 TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 540
TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVK+AESQIRDVDFA

Sbjct: 480 TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKSAESQIRDVDFA 539

Query: 541 SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ

Sbjct: 540 SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 574

Score = 875 bits (2262), Expect = 0.0
Identities = 468/558 (83%), Positives = 484/558 (85%), Gaps = 1/558 (0%)

Query: 550 NILAQSGSYAMAQANSSQ 567
NILAQSGSYAMAQANSSQ
Sbjct: 540 NILAQSGSYAMAQANSSQ 557

Score = 874 bits (2259), Expect = 0.0
Identities = 467/558 (83%), Positives = 484/558 (86%), Gaps = 1/558 (0%)

Query: 10 ALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLGQAIISNGND 69
ALNAKANSDLNAKSLD+SL+RLSSGLRINSAADDASGMAIADSLRSQANTLGQAIISNGND
Sbjct: 1 ALNAKANSDLNAKSLDSSLARLSSGLRINSAADDASGMAIADSLRSQANTLGQAIISNGND 60

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Query: 70  ALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLMEELDNIANTT 129
          ALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLMEELDNIANTT
Sbjct: 61  ALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLMEELDNIANTT 120

Query: 130 SFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSFTSGVVGLTI 189
          SFNGKQLLSG FTNQEFQIG+SSNQTVKATIGATQSSKIGVTRFETG+QSFTSG+VGLTI
Sbjct: 121 SFNGKQLLSGGFTNQEFQIGSSNQTVKATIGATQSSKIGVTRFETGSQSFTSGIVGLTI 180

Query: 190 KNYNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVRATYDVKTTGVYAIKEGTTT 249
          KNYNGIEDFKFDNVVISTSVGTGLGALAEINK+ADKTGVRATYDVKTTG YAIK GTTS
Sbjct: 181 KNYNGIEDFKFDNVVISTSVGTGLGALAEINKNADKTGVRATYDVKTTGAYAIKAGTTT 240

Query: 250 QDFAINGVTIGKIEYKDGNGSLISAINAVKDTTGVQASKDENGKLVLTSAADGRGIKIT 309
          QDFAINGV IGK++YKGD NGSLISAINAVKDTTGVQASKDENGKLVLTSAADGRGIKIT
Sbjct: 241 QDFAINGVIIIGVDYKDGNNGSLISAINAVKDTTGVQASKDENGKLVLTSAADGRGIKIT 300

Query: 310 GDIGVGSGILANQKENYGRSLVKNDGRDINISGTNLSAIGMGTTDMISQSSVSLRESKG 369
          GDIGVGSGIL QKENYGRSLVKNDGRDIN+SGT LSAIMG DMISQ+SVSLRESKG
Sbjct: 301 GDIGVGSGILFTQKENYGRSLVKNDGRDINVS GTGLSAIGMGADMISQASVSLRESKG 360

Query: 370 QISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXXXXKNLXXXXX 429
          QISA NADAMGFNSY GGG Q SSISAFM K+
Sbjct: 361 QISAANADAMGFNSYNGGGAKQILQ-ASSISAFMSQAGSGFSAGSGFSAGSGKDYSTILS 419

Query: 430 XXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXXXQFAALKTTAANTTDETAGVTTLKGAMAVM 489
          +TYV+ QFAALKT+ + + TAGVTTLKGAMAVM
Sbjct: 420 GSVQIVSSTASMSSTYVISEGSGFSAGSGNSQFAALKTSTVSAHEATAGVTTLKGAMAVM 479

Query: 490 DIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFASESANYSKA 549
          DIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVK+AESQIRDVDFASESANYSKA
Sbjct: 480 DIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKSAESQIRDVDFASESANYSKA 539

Query: 550 NILAQSGSYAMAQANSSQ 567
          NILAQSGSYAMAQANSSQ
Sbjct: 540 NILAQSGSYAMAQANSSQ 557

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sp      P27053          Flagellin A [flaA] [Campylobacter coli] 572 AA
        FLAA_CAMCO          align

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Score = 873 bits (2256), Expect = 0.0

Identities = 466/577 (80%), Positives = 495/577 (85%), Gaps = 7/577 (1%)

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Query: 1  GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
          GFRINTNVAALNAKANSDLN+++LD SLSRLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 1  GFRINTNVAALNAKANSDLNSRALDQSLRLSSGLRINSAADDASGMAIADSLRSQANTL 60

Query: 61 GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
          GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LME
Sbjct: 61 GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120

Query: 121 ELDNIANTTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
          ELDNIANTTTSFNGKQLLSG FTNQEFQIG+SSNQTVKATIGATQSSKIGVTRFETG+QSF
Sbjct: 121 ELDNIANTTTSFNGKQLLSGGFTNQEFQIGSSNQTVKATIGATQSSKIGVTRFETGSQSF 180

Query: 181 TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVRATYDVKTTGV 240

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+SG VGLTIKNGYNGIEDFKFD+VVISTSVGTGLGALAEIN++ADKTG+RAT+DVK+ G
Sbjct: 181 SSGTVGLTIKNGYNGIEDFKFDSVVISTSVGTGLGALAEINRNADKTGIRATFDVKSVA 240

Query: 241 YAIKEGTTSDFAINGVTIGKIEYKDGNGSLISAINAVKDTTGVQASKDENGKLVLT 300
YAIK G TSQDFAINGV IGK++Y DGD NGSLISAINAVKDTTGVQASKDENGKLVLT
Sbjct: 241 YAIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLVLT 300

Query: 301 ADGRGIKITGDIGVSGILANQKENYGRSLSVKNDGRDINISGTNLSAIGMGTTDMISQS 360
ADGRGIKITG IGVG+GIL ENYGRSLSVKNDGRDINISGT LSAIGMG TDMISQS
Sbjct: 301 ADGRGIKITGSIGVGAGIL--HTENYGRSLSVKNDGRDINISGTGLSAIGMGATDMISQS 358

Query: 361 SVSLRESKGQISATNADAMGFNSYKGGG--KFVFTQNVSSISAFMXXXXXXXXXXXXXXXXX 418
SVSLRESKGQISA NADAMGFN+Y GGG + +F SSI+ FM
Sbjct: 359 SVSLRESKGQISAAANADAMGFNAYNGGGAKQIIF--ASSIAGFMSQAGSGFSAGSGFSV 415

Query: 419 XXXKNLXXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXXXQFAALKTTAANTTDETAG 478
KN +TYVV QFAAL+ + + DETAG
Sbjct: 416 GSGKNYSAILSASIQIVSSARSISSTYVVSTGSGFSAGSGNSQFAALRISTVSAHDETAG 475

Query: 479 VTTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVD 538
VTTLKGAMAVMDIAETAITNLDQIRADIGS+QNQ+TSTINNITVTQVNVK+AESQIRDVD
Sbjct: 476 VTTLKGAMAVMDIAETAITNLDQIRADIGSVQNQITSTINNITVTQVNVKSAESQIRDVD 535

Query: 539 FASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
FASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ
Sbjct: 536 FASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 572

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tr Q84IB9 **Flagellin (Fragment) [flaA] [Campylobacter jejuni]** 572 AA
align

Score = 863 bits (2229), Expect = 0.0

Identities = 461/577 (79%), Positives = 491/577 (84%), Gaps = 7/577 (1%)

```

Query: 1 GFRINTNVAALNAKANSDLNNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
GFRINTN AALNAKANSDLN+++LD SLSRLSSGLRINSAADDASGMAIADSLRSQANT+
Sbjct: 1 GFRINTNGAALNAKANSDLNSRALDQSLRSLSSGLRINSAADDASGMAIADSLRSQANTM 60

Query: 61 GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
GQAISNG+DALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LME
Sbjct: 61 GQAISNGDDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120

Query: 121 ELDNIANTTTFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
ELDNIANTTTFNGKQLLSG FTNQEFQJG+SSNQT+KA+IGATQSSKIGVTRFETG+QSF
Sbjct: 121 ELDNIANTTTFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 180

Query: 181 TSGVVGLTIKNGYNGIEDFKFDNVVISTSVGTGLGALAEIN+ADKTG+RAT+DVK+ G 240
+SG VGLTIKNGYNGIEDFKF NVVISTSVGTGLGALAEIN++ADKTG+RAT+DVK+ G
Sbjct: 181 SSGTVGLTIKNGYNGIEDFKFQNVVISTSVGTGLGALAEINRNADKTGIRATFDVKSVA 240

Query: 241 YAIKEGTTSDFAINGVTIGKIEYKDGNGSLISAINAVKDTTGVQASKDENGKLVLT 300
Y IK G TSQDFAINGV IGK++Y DGD NGSLISAINAVKDTTGVQASKDENGKLVLT
Sbjct: 241 YTIKAGNTSQDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLVLT 300

Query: 301 ADGRGIKITGDIGVSGILANQKENYGRSLSVKNDGRDINISGTNLSAIGMGTTDMISQS 360
ADGRGIKITG IGVG+GIL ENYGRSLSVKN GRDINISGT LSAIGMG TDMISQS

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Sbjct: 301 ADGRGIKITGSIGVGAGIL--HTENYGRSLVKNVGRDINISGTGLSAIGMGATDMISQS 358
Query: 361 SVSLRESKGQISATNADAMGFNSYKGGG--KFVFTQNVSSISAFMXXXXXXXXXXXXXXXXX 418
SVSLRESKGQISA NADAMGFN+Y GGG + +F SSI+ FM
Sbjct: 359 SVSLRESKGQISAANADAMGFNAYNGGGAQIIIF--ASSIAGFMSQAGSGFSAGSGFSV 415
Query: 419 XXXKNLXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXXXQFAALKTTAANTTDETAG 478
KN +TYVV QFAAL+ + + DETAG
Sbjct: 416 GSGKNYSAILSASIQIVSSAASISSTYVVSAGSGFSAGSGNSQFAALRISTVSAHDETAG 475
Query: 479 VTTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVD 538
VTTLKGAMAVMDIAETAITNLDQIRADIGS+QNQ+TSTINNITVTQVNVK+AESQIRDVD
Sbjct: 476 VTTLKGAMAVMDIAETAITNLDQIRADIGSVQNQITSTINNITVTQVNVKSAESQIRDVD 535
Query: 539 FASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
FASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ
Sbjct: 536 FASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 572

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tr Q46009 Flagellin [Campylobacter coli] 572 AA
align

```

Score = 848 bits (2191), Expect = 0.0
Identities = 456/577 (79%), Positives = 487/577 (84%), Gaps = 8/577 (1%)

```

Query: 1 GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
GFRINTNVAALNAKANSDLN+++LD SLSRLSSGLRINSAAD ASGMAIADSLRSQANTL
Sbjct: 2 GFRINTNVAALNAKANSDLNSRALDQSLRSLSSGLRINSAADVASGMAIADSLRSQANTL 61
Query: 61 GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAA+DGQSLKTRTMLQADIN+LME
Sbjct: 62 GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAEDGQSLKTRTMLQADINRLME 121
Query: 121 ELDNIAINTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
ELDNIAINTTSFNGKQLLSG FTNQEFQIG+SSNQ+KA+IGATQSSKIGVTR + F
Sbjct: 122 ELDNIAINTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRLNRFTK-F 180
Query: 181 TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEIINKSADKTGVRATYDVKTTGV 240
+SG VGLTIKNYNGIEDFKFD+VVISTSVGTGLGALAEIIN++ADKTG+RAT+D+K+ G
Sbjct: 181 SSGTVGLTIKNYNGIEDFKFDSVVISTSVGTGLGALAEIINRNADKTGIRATFDLKSVA 240
Query: 241 YAIKEGTTSDFAINGVTIGKIEYKDGNGSLISAINAVKDTTGVQASKDENGKLV LTS 300
YAIK G TSQDFAINGV IKG++Y DGD NGSLISAINAVKDTTGVQASKDENGKLV LTS
Sbjct: 241 YAIKAGNTSDFAINGVVIGKVDYSDGDENGSLISAINAVKDTTGVQASKDENGKLV LTS 300
Query: 301 ADGRGIKITGDIGVSGILANQKENYGRSLVKN DGRDINISGTNLSAIGMGTTDMISQS 360
ADGRGIKITG IGVG+GIL ENYGRSLVKN DGRDINISGT SAIGMG TDMISQS
Sbjct: 301 ADGRGIKITGSIGVGAGIL--HTENYGRSLVKN DGRDINISGTGFS AIGMGATDMISQS 358
Query: 361 SVSLRESKGQISATNADAMGFNSYKGGG--KFVFTQNVSSISAFMXXXXXXXXXXXXXXXXX 418
SVSLRESKGQISA NADAMGFN+Y GGG + +F SSI+ FM
Sbjct: 359 SVSLRESKGQISAANADAMGFNAYNGGGAQIIIF--ASSIAGFMSQAGSGFSAGSGFSV 415
Query: 419 XXXKNLXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXXXQFAALKTTAANTTDETAG 478
KN +TYVV QFAAL+ + + DETAG
Sbjct: 416 GSGKNYSAILSASIQIVSSAASISSTYVVSTGSGFSAGSGNSQFAALRISTVSAHDETAG 475

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Query: 479 VTTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVD 538
VTTLKGAMAVMDIAETAITNLDQIRADIGS+QNQ+TSTINNITVTQVNVK+AESQIRDVD
Sbjct: 476 VTTLKGAMAVMDIAETAITNLDQIRADIGSVQNQITSTINNITVTQVNVKSAESQIRDVD 535

Query: 539 FASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
FASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ
Sbjct: 536 FASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 572

sp P18245 **Flagellin B (Flagellin N) [flaB] [Campylobacter coli]** 572 AA
FLAB_CAMCO

align

Score = 837 bits (2162), Expect = 0.0
Identities = 447/577 (77%), Positives = 482/577 (83%), Gaps = 7/577 (1%)

Query: 1 GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
GFRINTN+ ALNA ANS +NA+ LD SLSRLSSGLRINSAADDASGMAIADSLRSQA TL
Sbjct: 1 GFRINTNIGALNAHANSVFNARELDKSLRLSSGLRINSAADDASGMAIADSLRSQAATL 60

Query: 61 GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
GQAI+NGNDA+GILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LME
Sbjct: 61 GQAINNGNDAIGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120

Query: 121 ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
ELDNIANTTSFNGKQLLSG FTNQEFQIG+SSNQ+KA+IGATQSSKIGVTRFETG+QSF
Sbjct: 121 ELDNIANTTSFNGKQLLSGGFTNQEFQIGSSSNQTIKASIGATQSSKIGVTRFETGSQSF 180

Query: 181 TSGVVGLTIKNGYIEDFKFDNVVISTSVGTGLGALAEIINKSADKTGVRATYDVKTGTV 240
+SG VGLTIKNGYIEDFKFD+VVISTSVGTGLGALAEIIN++ADKTG+RAT+DVK+ G
Sbjct: 181 SSGTVGLTIKNGYIEDFKFDSVVISTSVGTGLGALAEIINRNADKTGIRATFDVKSVGA 240

Query: 241 YAIKEGTTSQDFAINGVTIGKIEYKDGNGSLISAINAVKDTTGVQASKDENGKLV LTS 300
YAIK G TSQDFAINGV IG+I Y DGD NG LISAINAVKDTTGVQASKDENGKLV LTS
Sbjct: 241 YAIKAGNTSQDFAINGVVIGQINYNDDGNGQLISAINAVKDTTGVQASKDENGKLV LTS 300

Query: 301 ADGRGIKITGDIGVSGILANQKENYGRSLSVKNDGRDINISGTNLSAIGMGTTDMISQS 360
ADGRGIKITG IGVG+GIL ENYGRSLSVKNDGRDINISGT LSAIGMG TDMISQS
Sbjct: 301 ADGRGIKITGSIGVGAGIL--HTENYGRSLSVKNDGRDINISGTGLSAIGMGATDMISQS 358

Query: 361 SVSLRESKGQISATNADAMGFNSYKGGG--KFVFTQNVSSISAFMXXXXXXXXXXXXXXXXX 418
SVSLRESKGQISA NADAMGFN+Y GGG + +F SSI+ FM
Sbjct: 359 SVSLRESKGQISAAANADAMGFNAYNGGGAKQIIF--ASSIAGFMSQAGSGFSAGSGFSV 415

Query: 419 XXXKNLXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXXXQFAALKTTAANTTDETAG 478
KN +TYVV QFAAL+ + + DETAG
Sbjct: 416 GSGKNYSAILSASIQIVSSARSISSTYVVSTGSGFSAGSGNSQFAALRISTVSAHDETAG 475

Query: 479 VTTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVD 538
VTTLKGAMAVMDIAETAITNLDQIRADIG++QNQ+ TINNITVTQVNVKAAES IRDVD
Sbjct: 476 VTTLKGAMAVMDIAETAITNLDQIRADIGAVQNQLQVTINNITVTQVNVKAAESTIRDVD 535

Query: 539 FASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
FA+ESAN+SK NILAQSGSYAM+Q N+ QQNVL+LLQ
Sbjct: 536 FAAESANFSKYNILAQSGSYAMSQRNAVQQNVLKLQ 572

sp Q46113 **Flagellin A [flaA] [Campylobacter jejuni]** 574 AA
FLA3_CAMJE align

Score = 803 bits (2075), Expect = 0.0
 Identities = 437/578 (75%), Positives = 472/578 (81%), Gaps = 7/578 (1%)

Query: 1 GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
 GFRINTNVAALNAKAN+DLN+KSLDASLSRLSSGLRINSAADDASGMAI DSLRSQANTL
 Sbjct: 1 GFRINTNVAALNAKANADLNSKSLDASLSRLSSGLRINSAADDASGMAIKDSLRSQANTL 60

Query: 61 GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
 GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LME
 Sbjct: 61 GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120

Query: 121 ELDNIAINTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
 ELDNIAINTTSFNGKQLLSGNF NQEFQIGASSNQTVKA+IGATQSSKIG+TRFETG++
 Sbjct: 121 ELDNIAINTTSFNGKQLLSGNFINQEFQIGASSNQTVKASIGATQSSKIGLTRFETGSRIS 180

Query: 181 TSGVVGLTIKKNYNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVRATYDVKTGTGV 240
 G V T+KNYNGI+DFKF VVISTSVGTGLGALA+EINK+ADKTGVRAT+ V+T G+
 Sbjct: 181 VGGEVQFTLKNYNGIDDFKFQKVISTSVGTGLGALADEINKNADKTGVRATFTVETGRM 240

Query: 241 YAIKEGTTSDFAINGVTIGKIEYKDGNGSLISAINAVKDTTGVQASKDENGKLVLT 300
 A++ G TS DFAINGV IGK++YKGDG NG+L+SAIN+VKDTTGV+AS DENGKL+LTS
 Sbjct: 241 GAVRAGATSDFAINGVKIGKVDYKGDANGALVSAINSVKDTTGVVEASIDENGKLLLT 300

Query: 301 ADGRGIKITGDIGVGSILANQKENYGRSLVKNDRDINISGTNLSAIGMGTTDMISQS 360
 +GRGIKI G+IG G+ I N ENYGRSLVKNDRG+DI ISGTNLSAIG GT +MISQ+
 Sbjct: 301 REGRIKIEGNIGRGAFINPNMLENYGRSLVKNDRGKDILISGTNLSAIGFGTGNMISQA 360

Query: 361 SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXX 420
 SVSLRESKGQI A ADAMGFNS G SS+SA+M
 Sbjct: 361 SVSLRESKGQIDANVADAMGFNSANKGN---ILGGYSSVSAYMSSTGSGFSSGSGFSVGS 417

Query: 421 XKNLXXXXXXXXXXXXXXXXXXNTYVXXXXXXXXXXXXXXXXXQFAALKTTAANT---TDETA 477
 KN Y V QFA +KT+A NT DETA
 Sbjct: 418 GKNYSTGFANTIAISAASQLSA-VYNVSAGSGFSSGSNLSQFATMKTSAGNTLGVKDETA 476

Query: 478 GVTTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDV 537
 GVTTLKGAMAVMDIAETAITNLDQIRADIGS+QNQVTSTINNITVTQVNVKAAESQIRDV
 Sbjct: 477 GVTTLKGAMAVMDIAETAITNLDQIRADIGSVQNQVTSTINNITVTQVNVKAAESQIRDV 536

Query: 538 DFASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
 DFA+ESANYSKANILAQSGSYAMAQANS QQNVLRLLQ
 Sbjct: 537 DFAAESANYSKANILAQSGSYAMAQANSVQQNVLRLLQ 574

tr Q84IB8 **Flagellin (Fragment) [flaA] [Campylobacter jejuni]** 575 AA
align

Score = 802 bits (2072), Expect = 0.0
 Identities = 433/578 (74%), Positives = 471/578 (80%), Gaps = 6/578 (1%)

```

Query: 1   GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
          GFRINTN AALNAKAN+DLN+KSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 1   GFRINTNGAALNAKANADLNSKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60

Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDITIKTKATQAAQDGQSLKTRTMLQADINKLME 120
          GQAISNGNDALGILQTADKAMDEQLKILDITIKTKATQAAQDGQSLKTRTMLQADIN+LME
Sbjct: 61  GQAISNGNDALGILQTADKAMDEQLKILDITIKTKATQAAQDGQSLKTRTMLQADINRLME 120

Query: 121 ELDNIANTTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
          ELDNIANTTTSFNGKQLLSGNF NQEFQIGASSNQTVKATIGATQSSKIG+TRFETG +
Sbjct: 121 ELDNIANTTTSFNGKQLLSGNFINQEFQIGASSNQTIKATIGATQSSKIGLTRFETGGRIS 180

Query: 181 TSGVVGLTIKKNYNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVRATYDVKTGTGV 240
          TSG V T+KNYNGI+DF+F VVISTSVGTGLGALA+EINK+ADKTGVRAT+ V+T G+
Sbjct: 181 TSGEVQFTLKNYNGIDDFQFQKVISTSVGTGLGALADEINKNADKTGVRATFTVETRGI 240

Query: 241 YAIKEGTTSDFAINGVTIGKIEYKDGNGSLISAINAVKDTTGVQASKDENGKLVLT 300
          A++ G TS DFAINGV IKG++YKGDG NG+L+SAIN+VKDTTGV+AS D NG+L+LTS
Sbjct: 241 AAVRAGATSDDFAINGVKIGKVDYKDGDSNGALVSAINSVKDTTGVVEASIDANGQLLLTS 300

Query: 301 ADGRGIKITGDIGVSGILANQKENYGRSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
          +GRGIKI G+IG G+ I A+ KENYGRSLVKNDG+DI ISGTNLS+ G G T ISQ+
Sbjct: 301 REGRGIKIDGNIGGGAFINASMKENYGRSLVKNDGKDILISGTNLSAGFGATQFISQA 360

Query: 361 SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXX 420
          SVSLRESKGQI A ADAMGF S G V SS++A+M
Sbjct: 361 SVSLRESKGQIDANIADAMGFGSVNKG---VMLGGFSSVTAYMSSAGSGFSAGSGYSVGS 417

Query: 421 XKNLXXXXXXXXXXXXXXXXXNTYVXXXXXXXXXXXXXXXXXQFAALKTTAANT---TDETA 477
          KN Y V QFA +KT+A N+ DETA
Sbjct: 418 GKNYSTSISGIAVAFSSGSLSAVINVSAGSGFSSQSGLSQFATMKTSAGNSLGVKDETA 477

Query: 478 GVTTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDV 537
          GVTTLKGAMAVMDIAETAITNLDQIRADIGS+QNQVTSTINNITVTQVNVKAAESQIRDV
Sbjct: 478 GVTTLKGAMAVMDIAETAITNLDQIRADIGSVQNQVTSTINNITVTQVNVKAAESQIRDV 537

Query: 538 DFASESANYSKANILAQSGSYAMAQANSSQQNVRLRLQ 575
          DFASESANYSKANILAQSGSYAMAQANS QQNVRLRLQ
Sbjct: 538 DFASESANYSKANILAQSGSYAMAQANSVQQNVRLRLQ 575

```

```

tr   Q9R952      Flagellin A [flaA] [Campylobacter jejuni]      572 AA
                                align

```

Score = 801 bits (2068), Expect = 0.0
Identities = 432/575 (75%), Positives = 470/575 (81%), Gaps = 4/575 (0%)

```

Query: 1   GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
          GFRINTNVAALNAKAN+DLN+KSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 2   GFRINTNVAALNAKANADLNSKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 61

Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDITIKTKATQAAQDGQSLKTRTMLQADINKLME 120
          GQAISNGNDALGILQTADKAMDEQLKILDITIKTKATQAAQDGQSLKTRTMLQADIN+LME
Sbjct: 62  GQAISNGNDALGILQTADKAMDEQLKILDITIKTKATQAAQDGQSLKTRTMLQADINRLME 121

Query: 121 ELDNIANTTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180

```

```

ELDNIANTTSFNGKQLLSGNF NQEFQIGASSNQTVKATIGATQSSKIG+TRFETG +
Sbjct: 122 ELDNIANTTSFNGKQLLSGNFINQEFQIGASSNQTVKATIGATQSSKIGLRFETGGRIS 181

Query: 181 TSGVVGLTIKKNYNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVRATYDVKTGGV 240
+SG V T+KNYNGI+DF+F VVISTSVGTGLGALA+EINK+ADKTGVRAT+ V+T G+
Sbjct: 182 SSGEVQFTLKNYNGIDDFQFQKVISTSVGTGLGALAEINKNADKTGVRATFTVETRGI 241

Query: 241 YAIKEGTTSDFAINGVTIGKIEYKDGNGSLISAINAVKDTTGVQASKDENGKLVLTLS 300
A++ G TS DFAINGV IGK++YKGDG NG+L++AIN+VKDTTGV+AS D NG+L+LTS
Sbjct: 242 AAVRAGATSDFAINGVKIGKVDYKGDANGALVAAINSVKDTTGVVEASIDANGQLLLTS 301

Query: 301 ADGRGIKITGDIGVSGILANQKENYGRSLVKNKNDGRDINISGTNLSAIGMGTTDMISQS 360
+GRGIKI G+IG G+ I A+ KENYGRSLVKNKNDG+DI ISG+NLS+ G G T ISQ+
Sbjct: 302 REGRGIKIDGNIGGGAFINADMKENYGRSLVKNKNDGKDILISGSNLSSAGFGATQFISQA 361

Query: 361 SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXX 420
SVSLRESKGQI A ADAMGF S K V SS+SA+M
Sbjct: 362 SVSLRESKGQIDANIADAMGFGS---ANKGVVLGGYSSVSAYMSSAGSGFSSGSGYSVGS 418

Query: 421 XKNLXXXXXXXXXXXXXXXXXXXXNTYVYVXXXXXXXXXXXXXXXXXQFAALKTTAANTTDETAGVT 480
KN Y V QFA +KTTA DETAGVT
Sbjct: 419 GKN-YSTGFANAIAISAASQLSTVYNVSAGSGFSSGSTLSQFATMKTTAFGVKDETAGVT 477

Query: 481 TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 540
TLKGAMAVMDIAETAITNLDQIRADIGS+QNQVTSTINNITVTQVNVKAAESQIRDVDFA
Sbjct: 478 TLKGAMAVMDIAETAITNLDQIRADIGSVQNQVTSTINNITVTQVNVKAAESQIRDVDFA 537

Query: 541 SESANYSKANILAQSGSYAMAQANSSQQNVRLRLQ 575
+ESANYSKANILAQSGSYAMAQANS QQNVRLRLQ
Sbjct: 538 AESANYSKANILAQSGSYAMAQANSVQQNVRLRLQ 572

```

```

sp      P56963          Flagellin A [flaA] [Campylobacter jejuni] 571 AA
        FLA1_CAMJE          align

```

Score = 800 bits (2065), Expect = 0.0

Identities = 432/575 (75%), Positives = 469/575 (81%), Gaps = 4/575 (0%)

```

Query: 1  GFRINTNVAALNAKANSDLNKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
GFRINTNVAALNAKAN+DLN+KSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 1  GFRINTNVAALNAKANADLNSKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60

Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDQGQSLKTRTMLQADINKLME 120
GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDQGQSLKTRTMLQADIN+LME
Sbjct: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDQGQSLKTRTMLQADINRLME 120

Query: 121 ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
ELDNIANTTSFNGKQLLSGNF NQEFQIGASSNQTVKATIGATQSSKIG+TRFETG +
Sbjct: 121 ELDNIANTTSFNGKQLLSGNFINQEFQIGASSNQTVKATIGATQSSKIGLRFETGGRIS 180

Query: 181 TSGVVGLTIKKNYNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVRATYDVKTGGV 240
TSG V T+KNYNGI+DF+F VVISTSVGTGLGALA+EINK+ADKTGVRAT+ V+T G+
Sbjct: 181 TSGEVQFTLKNYNGIDDFQFQKVISTSVGTGLGALAEINKNADKTGVRATFTVETRGI 240

Query: 241 YAIKEGTTSDFAINGVTIGKIEYKDGNGSLISAINAVKDTTGVQASKDENGKLVLTLS 300
A++ G TS FAINGV IGK++YKGDG NG+L++AIN+VKDTTGV+AS D NG+L+LTS

```

```

Sbjct: 241 AAVRAGATSDTFAINGVKIGKVDYKGDANGALVAAINSVKDTTGVASIDANGQLLLTS 300

Query: 301 ADGRGIKITGDIGVSGILANQKENYGRSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
      +GRGIKI G+IG G+ I A+ KENYGRSLVKNDG+DI ISG+NLS+ G G T ISQ+
Sbjct: 301 REGRGIKIDGNIGGGAFINADMKENYGRSLVKNDGKDILISGSNLSSAGFGATQFISQA 360

Query: 361 SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXX 420
      SVSLRESKGQI A ADAMGF S K V SS+SA+M
Sbjct: 361 SVSLRESKGQIDANIADAMGFGS---ANKGVVLGGYSSVSAYMSSAGSGFSSGSGYSVGS 417

Query: 421 XKNLXXXXXXXXXXXXXXXXXXNTYVXXXXXXXXXXXXXXXXXXQFAALKTTAANTTDETAGVT 480
      KN Y V QFA +KTTA DETAGVT
Sbjct: 418 GKN-YSTGFANAIAISAASQLSTVYNVSAGSGFSSGSTLSQFATMKTTAFGVKDETAGVT 476

Query: 481 TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 540
      TLKGAMAVMDIAETAITNLDQIRADIGS+QNQVTSTINNITVTQVNVKAAESQIRDVDFA
Sbjct: 477 TLKGAMAVMDIAETAITNLDQIRADIGSVQNQVTSTINNITVTQVNVKAAESQIRDVDFA 536

Query: 541 SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
      +ESANYSKANILAQSGSYAMAQANS QQNVLRLLQ
Sbjct: 537 AESANYSKANILAQSGSYAMAQANSVQQNVLRLLQ 571

```

```

tr    O85182      Flagellin A [flaA] [Campylobacter jejuni]      572 AA
                                align

```

Score = 796 bits (2057), Expect = 0.0

Identities = 431/575 (74%), Positives = 468/575 (80%), Gaps = 4/575 (0%)

```

Query: 1  GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
      GFRINTNVAALNAKAN+DLN+KSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 2  GFRINTNVAALNAKANADLNSKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 61

Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDITIKTKATQAAQDGQSLKTRTMLQADINKLME 120
      GQAISNGNDALGILQTADKAMDEQLKILDITIKTKATQAAQDGQSLKTRTMLQADIN+LME
Sbjct: 62  GQAISNGNDALGILQTADKAMDEQLKILDITIKTKATQAAQDGQSLKTRTMLQADINRLME 121

Query: 121  ELDNIANTTTFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
      ELDNIANTTTFNGKQLLSGNF NQEFQIGASSNQTVKATIGATQSSKIG+TRFETG +
Sbjct: 122  ELDNIANTTTFNGKQLLSGNFINQEFQIGASSNQTVKATIGATQSSKIGLTRFETGGRIS 181

Query: 181  TSGVVGLTIKKNYNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVRATYDVKTGTV 240
      +SG V T+KNYNGI+DF+F VVISTSVGTGLGALA+EINK+ADKTGVRAT+ V+T G+
Sbjct: 182  SSGEVQFTLKNYNGIDDFQFQKVVISTSVGTGLGALADEINKNADKTGVRATFTVETRGI 241

Query: 241  YAIKEGTTSDFAINGVTIGKIEYKGDGNGSLISAINAVKDTTGVQASKDENGKLVLT 300
      A++ G TS FAINGV IKG++YKGDG NG+L++AIN+VKDTTGV+AS D NG+L+LTS
Sbjct: 242  AAVRAGATSDTFAINGVKIGKVDYKGDANGALVAAINSVKDTTGVASIDANGQLLLTS 301

Query: 301  ADGRGIKITGDIGVSGILANQKENYGRSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
      +GRGIKI G+IG G+ I A+ KENYGRSLVKNDG+DI ISG+NLS+ G G T ISQ+
Sbjct: 302  REGRGIKIDGNIGGGAFINADMKENYGRSLVKNDGKDILISGSNLSSAGFGATQFISQA 361

Query: 361  SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXX 420
      SVSLRESKGQI A ADAMGF S K V SS+SA+M
Sbjct: 362  SVSLRESKGQIDANIADAMGFGS---ANKGVVLGGYSSVSAYMSSAGSGFSSGSGYSVGS 418

```

```

Query: 421 XKNLXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXXXQFAALKTTAANTTDETAGVT 480
          KN                      Y V                      QFA  KTTA    DETAGVT
Sbjct: 419 GKN-YSTGFANAIAISAASQLSTVYNVSAGSGFSSGSTLSQFATKKTAFGVKDETAGVT 477

Query: 481 TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 540
          TLKGAMAVMDIAETAITNLDQIRADIGS+QNQVTSTINNITVTQVNVKAAESQIRDVDFA
Sbjct: 478 TLKGAMAVMDIAETAITNLDQIRADIGSVQNQVTSTINNITVTQVNVKAAESQIRDVDFA 537

Query: 541 SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
          +ESANYSKANILAQSGSYAMAQANS QQNVLRLLQ
Sbjct: 538 AESANYSKANILAQSGSYAMAQANSVQQNVLRLLQ 572

```

```

tr      Q9R949      Flagellin A [flaA] [Campylobacter jejuni]      572 AA
                                align

```

Score = 796 bits (2055), Expect = 0.0

Identities = 429/575 (74%), Positives = 468/575 (80%), Gaps = 4/575 (0%)

```

Query: 1   GFRINTNVAALNAKANSDLNKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
          GFRINTNVAALNAKAN+DLN+KSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 2   GFRINTNVAALNAKANADLNSKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 61

Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
          GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LME
Sbjct: 62  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 121

Query: 121 ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
          ELDNIANTTSFNGKQLLSGNF NQEFQIGASSNQTVKATIGATQSSKIG+TRFETG +
Sbjct: 122 ELDNIANTTSFNGKQLLSGNFINQEFQIGASSNQTVKATIGATQSSKIGLTRFETGGRIS 181

Query: 181 TSGVVGLTIKKNYNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVRATYDVKTGTV 240
          +SG V T+KNYNGI+DF+F VVISTSVGTGLGALA+EINK+ADKTGVRAT+ V+T G+
Sbjct: 182 SSGEVQFTLKNYNGIDDFQFQKVVISTSVGTGLGALADEINKNADKTGVRATFTTVETRGI 241

Query: 241 YAIKEGTTSDFAINGVTIGKIEYKDGNGSLISAINAVKDTTGVQASKDENGKLVLTLS 300
          A++ G TS DFAINGV IGK++YKDG NG+L++AIN+VKDTTGV+AS D NG+L+LTS
Sbjct: 242 AAVRAGATSDDFaingvKIGKVDYKDGANGALVAAINSVKDTTgveASIDANGQLLLTS 301

Query: 301 ADGRGIKITGDIGVSGILANQKENYGRSLSVKNDGRDINISGTNLSAIGMGTTDMISQS 360
          +GRGIKI G+IG G+ I A+ KENYGRSLSVKNDG+DI ISG+NLS+ G G T ISQ+
Sbjct: 302 REGRGIKIDGNIGGGAFINADMKENYGRSLSVKNDGKDILISGSNLSSAGFGATQFISQA 361

Query: 361 SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXX 420
          SVSLRESKG+ A ADAMGF S K V SS+SA+M
Sbjct: 362 SVSLRESKGRFDANIADAMGFGS---ANKGVVLGGYSSVSAYMSSAGSGFSSSGSYSVGS 418

Query: 421 XKNLXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXXXQFAALKTTAANTTDETAGVT 480
          KN                      Y V                      QFA +KTTA    DETAGVT
Sbjct: 419 GKN-YSTGFAKAIISAASQLSTVYNVSAGSGFSSGSTLSQFATMKTAFGVKDETAGVT 477

Query: 481 TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 540
          TLKGAMAVMDIAETA TNLDQIRADIGS+QNQVTSTINNITVTQVNVKAAESQIRDVDFA
Sbjct: 478 TLKGAMAVMDIAETATTNLDQIRADIGSVQNQVTSTINNITVTQVNVKAAESQIRDVDFA 537

```


Query: 541 SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
 +ESANYSKANILAQSGSYAMAQANS QQNVLRLLQ
 Sbjct: 538 AESANYSKANILAQSGSYAMAQANSVQQNVLRLLQ 572

tr 030696 **Flagellin A [flaA] [Campylobacter jejuni]** 576 AA
align

Score = 795 bits (2053), Expect = 0.0
 Identities = 429/578 (74%), Positives = 471/578 (81%), Gaps = 6/578 (1%)

Query: 1 GFRINTNVAALNAKANSDLNKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
 GFRINTNVAALNAKAN+DLN+KSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL
 Sbjct: 2 GFRINTNVAALNAKANADLNSKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 61

Query: 61 GQAISNGNDALGILQTADKAMDEQLKILDITIKTKATQAAQDGQSLKTRTMLQADINKLME 120
 GQAISNGNDALGILQTADKAMDEQLKILDITIKTKATQAAQDGQSLKTRTMLQA+IN+LME
 Sbjct: 62 GQAISNGNDALGILQTADKAMDEQLKILDITIKTKATQAAQDGQSLKTRTMLQANINRLME 121

Query: 121 ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
 ELDNIANTTSF+GKQLLSGNF NQEFQIGASSNQTVKATIGATQSSKIG+TRFETG +
 Sbjct: 122 ELDNIANTTSFSGKQLLSGNFINQEFQIGASSNQTVKATIGATQSSKIGLTRFETGERIS 181

Query: 181 TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVRATYDVKTGTV 240
 +SG V T+KNYNGI+DFKF VVISTSVGTGLGALA+EINK+ADKTGVRAT+ V+T G+
 Sbjct: 182 SSGEVQFTLKNYNGIDDFKFQKVISTSVGTGLGALADEINKNADKTGVRATFTVETRGM 241

Query: 241 YAIKEGTTSDFAINGVTIGKIEYKDGNGSLISAINAVKDTTGVQASKDENGKLVLT 300
 A++ GTTS DFAINGV IGK++YKGDG NG+L+SAIN+VKDTTGV+AS D NG+L+LTS
 Sbjct: 242 AAVRAGTTSDDFAINGVKIGKVDYKDGDSNGALVSAINSVKDTTGVVEASIDANGQLLLTS 301

Query: 301 ADGRGIKITGDIGVSGILANQKENYGRSLSVKNDGRDINISGTNLSAIGMGTTDMISQS 360
 +GRGIKI G+IG G+ I A+ KENYGRSLSVKNDG+DI ISG+NLS+ G G T SQ+
 Sbjct: 302 REGRGIKIEGNIGGGAFINASMKENYGRSLSVKNDGKDILISGSNLSSAGFGATQFTSQA 361

Query: 361 SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXX 420
 SVSLRESKGQI A ADAMGF S G K S+++A+M
 Sbjct: 362 SVSLRESKGQIDANIADAMGFGSVNKGVKL---SGFSTVTAYMSSAGSGFSAGSGYSVGS 418

Query: 421 XKNLXXXXXXXXXXXXXXXXXNTYVXXXXXXXXXXXXXXXXXQFAALKTTAANT---TDETA 477
 KN Y V QFA +KT+ N+ DETA
 Sbjct: 419 GKNYSTSISGIAVAFSSGSLSAEYNVSAGSGFSSQSGLSQFATMKTSVGNSLGVKDETA 478

Query: 478 GVTTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDV 537
 GVTTLKGAMAVMDIAETAITNLDQIRADIGS+QNQVTSTINNITVTQVNVKAAESQIRDV
 Sbjct: 479 GVTTLKGAMAVMDIAETAITNLDQIRADIGSVQNQVTSTINNITVTQVNVKAAESQIRDV 538

Query: 538 DFASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
 DFA+ESANYSKANILAQSGSYAMAQANS QQNVLRLLQ
 Sbjct: 539 DFAAESANYSKANILAQSGSYAMAQANSVQQNVLRLLQ 576

tr 030689 **Flagellin A [flaA] [Campylobacter jejuni]** 572 AA
align

Score = 794 bits (2050), Expect = 0.0
Identities = 428/575 (74%), Positives = 467/575 (80%), Gaps = 4/575 (0%)

```

Query: 1  GFRINTNVAALNAKANSDLNKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
          GFRINTNVAALNAKAN+DLN+KSLDASLSRLSSGLRINSAADDASGMAIAD+LRSQANTL
Sbjct: 2  GFRINTNVAALNAKANADLNSKSLDASLSRLSSGLRINSAADDASGMAIADTLRSQANTL 61

Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDITIKTKATQAAQDGQSLKTRTMLQADINKLME 120
          GQAISNGNDA+GILQTADKAMDEQLKILDITIKTKATQAAQDGQSLKTRTMLQADIN+LME
Sbjct: 62  GQAISNGNDAIGILQTADKAMDEQLKILDITIKTKATQAAQDGQSLKTRTMLQADINRLME 121

Query: 121  ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
          ELDNIANTTSFNGKQLLSGNF NQEFQIGASSNQTVKATIGATQSSKIG+TRFETG +
Sbjct: 122  ELDNIANTTSFNGKQLLSGNFINQEFQIGASSNQTVKATIGATQSSKIGLTRFETGGRIS 181

Query: 181  TSGVVGLTIKKNYNGIEDFKFDNVVISTSVGTGLGALAEIEINKSADKTGVRATYDVKTTGV 240
          TSG V T+KNYNGI+DF+F VVISTSVGTGLGALA+EINK+ADKTGVRAT+ V+T G+
Sbjct: 182  TSGEVQFTLKNYNGIDDFQFQKVISTSVGTGLGALADEINKNADKTGVRATFTVETRGI 241

Query: 241  YAIKEGTTSDFAINGVTIGKIEYKDGNGSLISAINAVKDTTGVQASKDENGKLVLT 300
          A++ G TS FAINGV IKG++YKGDG NG+L++AIN+VKDTTGV+AS D NG+L+LTS
Sbjct: 242  AAVRAGATSDTFAINGVKIGKVDYKGDANGALVAAINSVKDTTGVVEASIDANGQLLLTS 301

Query: 301  ADGRGIKITGDIGVSGILANQKENYGRSLSVKNDGRDINISGTNLSAIGMGTTDMISQS 360
          +GRGIKI G+IG G+ I A+ KENYGRSLSVKNDG+DI ISG+NLS+ G G T ISQ+
Sbjct: 302  REGRGIKIDGNIGGGAFINADMKENYGRSLSVKNDGKDILISGSNLSSAGFGATQFISQA 361

Query: 361  SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXXXX 420
          SVSLRESKGQI A ADAMGF S K V SS+SA+M
Sbjct: 362  SVSLRESKGQIDANIADAMGFGS---ANKGVVLGGYSSVSAYMSSAGSGFSSSGSGYSVGS 418

Query: 421  XKNLXXXXXXXXXXXXXXXXXXXXNTYVYVXXXXXXXXXXXXXXXXXXQFAALKTTAANTTDETAGVT 480
          KN Y V QFA +KTTA DETAGVT
Sbjct: 419  GKN-YSTGFANAIAISAASQLSTVYNVSAGSGFSSGSTLSQFATMKTTAFGVKDETAGVT 477

Query: 481  TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 540
          TLKGAMAVMDIAETA TNLDQIRADIGS+QNQVTSTINNITVTQVNVKAAESQIRDVDFA
Sbjct: 478  TLKGAMAVMDIAETATTNLDQIRADIGSVQNQVTSTINNITVTQVNVKAAESQIRDVDFA 537

Query: 541  SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
          +ESANYSKANILAQSGSYAMAQANS QNVLRLLQ
Sbjct: 538  AESANYSKANILAQSGSYAMAQANSVHQNVLRLLQ 572

```

tr Q8G9F2 **Flagellin (Fragment) [flaA] [Campylobacter jejuni]** 574 AA
align

Score = 793 bits (2049), Expect = 0.0
Identities = 430/578 (74%), Positives = 469/578 (80%), Gaps = 7/578 (1%)

```

Query: 1  GFRINTNVAALNAKANSDLNKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
          GFRINTN AALNAKAN+DLN+KSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 1  GFRINTNGAALNAKANADLNSKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60

Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDITIKTKATQAAQDGQSLKTRTMLQADINKLME 120
          GQAISNGNDALGILQTADKAMDEQLKILDITIKTKATQAAQDGQSLKTRTMLQADIN+LME

```

```

Sbjct: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120

Query: 121  ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
           ELDNIANTTSFNGKQLLSGNF NQEFQIGASSNQTVKATIGATQSSKIG+TRFETG +
Sbjct: 121  ELDNIANTTSFNGKQLLSGNFINQEFQIGASSNQTVKATIGATQSSKIGLTRFETGGRIS 180

Query: 181  TSGVVGLTIKNGYNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVRATYDVKTTGV 240
           +SG V T+KNYNGI+DFKF VVISTSVGTGLGALA+EINK+ADKTGVRAT+ V+T G+
Sbjct: 181  SSGEVQFTLKNYNGIDDFKFQKVISTSVGTGLGALADEINKNADKTGVRATFTVETRGM 240

Query: 241  YAIKEGTTSDFAINGVTIGKIEYKDGNGSLISAINAVKDTTGVQASKDENGKLVLT 300
           A++ GTTS+DF INGV IG+IEYKDG NG+L++AIN+VKDTTGV+AS D NGKL+LTS
Sbjct: 241  GAVRAGTTSEDFTINGVKIGQIEYKDGDSNGALVAAINSVKDTTGVVEASIDSNGLLLTS 300

Query: 301  ADGRGIKITGDIGVGSGILANQKENYGRSLSVKNDGRDINISGTLNLSAIGMGTTDMISQS 360
           +GRGIKI GDIG G+ I + KENYGRSLSVKNDG+DI ISG+NLS+ G G + ISQ+
Sbjct: 301  REGRGIKIEGDIGRGAFINPDMKENYGRSLSVKNDGKDILISGSLNLSAGFGANNFISQA 360

Query: 361  SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXX 420
           SVSLRESKGQ+ A ADAMGFNS G SS+ A+M
Sbjct: 361  SVSLRESKGQLDANVADAMGFNSVDKGN---ILGGYSSVQAYMSSAGSGFSSGSGYSVGS 417

Query: 421  XKNLXXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXXXQFAALKTTAANT---TDETA 477
           KN Y + QFA +KT+A N+ DETA
Sbjct: 418  GKNYSTGFANVVAVSAISQMSA-VYNISAGSGFSSGSTLSQFATMKTSAGNSLGVKDETA 476

Query: 478  GVTTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDV 537
           GVTTLKGAMAVMDI ETAITNLDQIRADIGS+QNQVTSTINNITVTQVNVKAAESQIRDV
Sbjct: 477  GVTTLKGAMAVMDIPETAITNLDQIRADIGSVQNQVTSTINNITVTQVNVKAAESQIRDV 536

Query: 538  DFASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
           DFASESANYSKANILAQSGSYAMAQANS QQNVLRLLQ
Sbjct: 537  DFASESANYSKANILAQSGSYAMAQANSVQQNVLRLLQ 574

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```

tr    034938          Flagellin A [flaA] [Campylobacter jejuni]          575 AA
                                           align

```

Score = 792 bits (2045), Expect = 0.0

Identities = 428/578 (74%), Positives = 467/578 (80%), Gaps = 7/578 (1%)

```

Query: 1    GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
           GFRINTNVAALNAKANSDLN+K+LD SL+RLSSGLRINSAADDASGMAIADSLRSQA+TL
Sbjct: 2    GFRINTNVAALNAKANSDLNSKALDQSLARLSSGLRINSAADDASGMAIADSLRSQASTL 61

Query: 61   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
           GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LME
Sbjct: 62   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 121

Query: 121  ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
           ELDNIANTTSFNGKQLLSGNF NQEFQIGASSNQTVK TIGATQSSKIG+TRFETG +
Sbjct: 122  ELDNIANTTSFNGKQLLSGNFINQEFQIGASSNQTVKTTIGATQSSKIGLTRFETGGRIS 181

Query: 181  TSGVVGLTIKNGYNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVRATYDVKTTGV 240
           SG V T+KNYNGI+DFKF VVISTSVGTGLGALA+EINK+ADKTGVRAT+ V+T G+
Sbjct: 182  ESGEVQFTLKNYNGIDDFKFQKVISTSVGTGLGALADEINKNADKTGVRATFTVETRGM 241

```

```

Query: 241 YAIKEGTTSDFAINGVTIGKIEYKDGNGSLISAINAVKDTTGVQASKDENGKLVLT 300
      A++EGTTS DF INGV IGK+EYKGDG NG+L++AIN+VKDTTGV+AS D NG+L+LTS
Sbjct: 242 GAVREGTTSDDFTINGVKIGKVEYKGDGNSGALVAAINSVKDTTGVVEASIDVNGQLLLTS 301

Query: 301 ADGRGIKITGDIGVGSILANQKENYGRSLVKN DGRDINISGTNLSAIGMGTTDMISQS 360
      +GRGIKI GDIG G+ I N KENYGRSLVKN D+DI ISGT L+A G G ISQ+
Sbjct: 302 REGRGIKIEGDIGRGAFINPNMKENYGRSLVKN DGDILISGTGLTATGFGVNSFISQA 361

Query: 361 SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXX 420
      SVSLRESKGQI A ADAMGFNS G SS+S++M
Sbjct: 362 SVSLRESKGQIDANVADAMGFNSVDKGN---ILGGFSSVSSYMSSAGSGFSSGSGFSVGS 418

Query: 421 XKNLXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXXXQFAALKTTAANT---TDETA 477
      KN Y + QFA +KT+ NT DETA
Sbjct: 419 GKNYSTGFANVVVVS AISQMSA-VYNISAGSGFSSQSGLSQFATMKTSVGNLTVKDETA 477

Query: 478 GVTTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDV 537
      GVTTLKGAMAVMDIAETAITNLDQIRADIGS+QNQ+TSTINNITVTQVNVK+AESQIRDV
Sbjct: 478 GVTTLKGAMAVMDIAETAITNLDQIRADIGSVQNQITSTINNITVTQVNVKSAESQIRDV 537

Query: 538 DFASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
      DFA+ESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ
Sbjct: 538 DFAAESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575

```

tr 085180 **Flagellin A [flaA] [Campylobacter jejuni]** 575 AA
align

Score = 785 bits (2027), Expect = 0.0
Identities = 425/578 (73%), Positives = 464/578 (79%), Gaps = 7/578 (1%)

```

Query: 1 GFRINTNVAALNAKANSDLNKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
      GFRINTN AALNAKAN+DLN+KSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 2 GFRINTNGAALNAKANADLNSKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 61

Query: 61 GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
      GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LME
Sbjct: 62 GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 121

Query: 121 ELDNIANTTTFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
      ELDNIANTTTFNGKQLLSGNF NQEFQIGASSNQTVKATIGATQSSKIG+TRFETG +
Sbjct: 122 ELDNIANTTTFNGKQLLSGNFINQEFQIGASSNQTVKATIGATQSSKIGLTRFETGGRIS 181

Query: 181 TSGVVGLTIKKNYNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVRATYDVKTGTG 240
      +SG V T+KNYNGI+DF+F VVISTSVGTGLGALA+EINK+ADKTGVRAT+ V+T G+
Sbjct: 182 SSGEVQFTLKNYNGIDDFQFQKVVISVSVGTGLGALADEINKNADKTGVRATFTVETGRM 241

Query: 241 YAIKEGTTSDFAINGVTIGKIEYKDGNGSLISAINAVKDTTGVQASKDENGKLVLT 300
      A++ GTTS DFAINGV IGK+ Y+DGD NG+L+SAIN+VKDTTGV+AS D NG+L+LTS
Sbjct: 242 AAVRAGTTSDDFAINGVKIGKVAYEDGDANGALVSAINSVKDTTGVVEASIDANGQLLLTS 301

Query: 301 ADGRGIKITGDIGVGSILANQKENYGRSLVKN DGRDINISGTNLSAIGMGTTDMISQS 360
      +GRGIKI G IG G+ I + ENYGRSLVKN D+DI+ISGT LS G G ++ ISQ
Sbjct: 302 REGRGIKIEGSIGGAFINKDMMENYGRSLVKN DGDIDISISGTGLSFTGFGASNFISQV 361

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Query: 361 SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXXXX 420
          SVSLRESKGQ+ A ADAMGF S G SSI+ +M
Sbjct: 362 SVSLRESKGQLDANTADAMGFGSVNKG----LVLAASSIADYMSAEGSGFSAGSGYSVGS 417

Query: 421 XKNLXXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXXXXQFAALKTTAANT---TDETA 477
          K Y V QFA +KT+A N+ DETA
Sbjct: 418 GKGYSATLTANAIAISSASAIISKIYNVSQSGFSSGSTLSQFATMKTSAGNSLGAKDETA 477

Query: 478 GVTTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDV 537
          GVTTLKGAMAVMDIAETAITNLDQIRADIGS+QNQVTSTINNITVTQVNVKAAESQIRDV
Sbjct: 478 GVTTLKGAMAVMDIAETAITNLDQIRADIGSVQNQVTSTINNITVTQVNVKAAESQIRDV 537

Query: 538 DFAESANYSKANILAQSGSYAMAQANSQQNVLRLLQ 575
          DFA+ESANYSKANILAQSGSYAMAQANS QQNVLRLLQ
Sbjct: 538 DFAAESANYSKANILAQSGSYAMAQANSVQQNVLRLLQ 575

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tr Q8G9F1 Flagellin (Fragment) [flaA] [Campylobacter coli] 574 AA
                                align

```

Score = 782 bits (2020), Expect = 0.0

Identities = 424/578 (73%), Positives = 463/578 (79%), Gaps = 7/578 (1%)

```

Query: 1 GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
          GFRINTN AALNAKAN+DLN+KSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 1 GFRINTNGAALNAKANADLNSKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60

Query: 61 GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
          GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LME
Sbjct: 61 GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120

Query: 121 ELDNIAINTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
          ELDNIAINTTSFNGKQLLSGNF NQEFQIGASSNQTVKATIGATQSSKIG+TRFETG +
Sbjct: 121 ELDNIAINTTSFNGKQLLSGNFINQEFQIGASSNQTVKATIGATQSSKIGLTRFETGGRIS 180

Query: 181 TSGVVGLTIKKNYNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVRATYDVKTTGV 240
          +SG V T+KNYNGI+DF+F VVISTSVGTGLGALA+EINK+ADKTGVRAT+ V+T G+
Sbjct: 181 SSGEVQFTLKNYNGIDDFQFQKVISTSVGTGLGALADEINKNADKTGVRATFTVETRGM 240

Query: 241 YAIKEGTTSDFAINGVTIGKIEYKDGNGSLISAINAVKDTTGVQASKDENGKLVLT 300
          A++ GTTS FAINGV IGK+ Y+DGD NG+L+SAIN+VKDTTGV+AS D NG+L+LTS
Sbjct: 241 AAVRAGTTSDTFAINGVKIGKVAYEDGDANGALVSAINSVKDTTGVVEASIDANGQLLLTS 300

Query: 301 ADGRGIKITGDIGVSGILANQKENYGRSLVKNKDGRDINISGTNLSAIGMGTTDMISQS 360
          +GRGIKI G IG G+ I + ENYGRSLVKNKNDG+DI+ISGT LS G G ++ ISQ
Sbjct: 301 REGRIKIEGSIGGGAFINKDMMENYGRSLVKNKNDGKDISISGTGLSFTGFGASNFISQV 360

Query: 361 SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXXXX 420
          SVSLRESKGQ+ A ADAMGF S G SSI+ +M
Sbjct: 361 SVSLRESKGQLDANTADAMGFGSVNKG----LVLAASSIADYMSAEGSGFSAGSGYSVGS 416

Query: 421 XKNLXXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXXXXQFAALKTTAANT---TDETA 477
          K Y V QFA +KT+A N+ DETA
Sbjct: 417 GKGYSTTLTANAIAISSASAIISKIYNVSQSGFSSGSTLSQFATMKTSAGNSLGAKDETA 476

Query: 478 GVTTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDV 537

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GVTTTLKGAMAVMDIAETAITNLDQIRADIGSVQNVVKAESQIRDV
 Sbjct: 477 GVTTTLKGAMAVMDIAETAITNLDQIRADIGSVQNVVKAESQIRDV 536

Query: 538 DFASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575

DFA+ESANYSKANILAQSGSYAMAQANS QQNVLRLLQ

Sbjct: 537 DFAAESANYSKANILAQSGSYAMAQANSVQQNVLRLLQ 574

sp Q46114 **Flagellin B [flaB] [Campylobacter jejuni]** 574 AA
 FLB3_CAMJE align

Score = 776 bits (2005), Expect = 0.0

Identities = 422/578 (73%), Positives = 464/578 (80%), Gaps = 7/578 (1%)

Query: 1 GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60

GFRINTN+ ALNA ANS +NA+ LD SLSRLSSGLRINSAADDASGMAIADSLRSQA TL

Sbjct: 1 GFRINTNIGALNAHANSVVNARELDKSLRLSSGLRINSAADDASGMAIADSLRSQAATL 60

Query: 61 GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120

GQAI+NGNDA+GILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LME

Sbjct: 61 GQAINNGNDAIGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 120

Query: 121 ELDNIAINTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180

ELDNIAINTTSFNGKQLLSGNF NQEFQIGASSNQ+KATIGATQSSKIG+TRFETG++

Sbjct: 121 ELDNIAINTTSFNGKQLLSGNFINQEFQIGASSNQTIKATIGATQSSKIGLTRFETGSRIS 180

Query: 181 TSGVVGLTIKKNYNGIEDFKFDNVVISTSVGTGLGALAEIINKSADKTGVRATYDVKTGGV 240

G V T+KNYNGI+DFKF VVISTSVGTGLGALAEIINKSAD+TGVRAT+ V+T G+

Sbjct: 181 VGGEVQFTLKNYNGIDDFKFQKVISTSVGTGLGALAEIINKSADQGTGVRATFTVETGRM 240

Query: 241 YAIKEGTTSDFAINGVTIGKIEYKDGNGSLISAINAVKDTTGVQASKDENGKLVLT 300

A++ G TS+DFAINGV IG+IEYKDG NG+L+SAIN+VKDTTGV+AS DENGKL+LTS

Sbjct: 241 GAVRAGATSEDFAINGVKIGQIEYKDGANGALVSAINSVKDTTGV+AS DENGKLLLT 300

Query: 301 ADGRGIKITGDIGVGSILANQKENYGRSLVKNDGRDINISGTNLSAIGMTTDMISQS 360

+GRGIKI G+IG G+ I N ENYGRSLVKNDG+DI ISGTNLSAIG GT +MISQ+

Sbjct: 301 REGRIKIEGNIGRGAFINPNMLENYGRSLVKNDGKDILISGTNLSAIGFGTGNMISQA 360

Query: 361 SVSLRESKGQISATNADAMGFNSYKGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXX 420

SVSLRESKGQI A ADAMGFNS G SS+SA+M

Sbjct: 361 SVSLRESKGQIDANVADAMGFNSANKGN---ILGGYSSVSAYMSSTGSGFSSGSGFSVGS 417

Query: 421 XKNLXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXQFAALKTTAANT---TDETA 477

KN Y V QFA +KT+A NT DETA

Sbjct: 418 GKNYSTGFANTIAISAASQLSA-VYNVSAGSGFSSGSNLSQFATMKTSAGNTLGVKDETA 476

Query: 478 GVTTTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQNVVKAESQIRDV 537

GVTTTLKGAMAVMDIAETAITNLDQIRADIGSVQNV+ TINNITVTQNVVKAES IRDV

Sbjct: 477 GVTTTLKGAMAVMDIAETAITNLDQIRADIGSVQNVQLQVTINNITVTQNVVKAESTIRDV 536

Query: 538 DFASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575

DFA+ESAN+SK NILAQSGSYAM+QAN+ QQNVL+LLQ

Sbjct: 537 DFAAESANFSKYNILAQSGSYAMSQANAVQQNVLKLQ 574

Score = 768 bits (1983), Expect = 0.0
Identities = 415/575 (72%), Positives = 457/575 (79%), Gaps = 4/575 (0%)

Score = 767 bits (1980), Expect = 0.0
Identities = 419/579 (72%), Positives = 459/579 (78%), Gaps = 8/579 (1%)

8/31/04

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Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDITIKTKATQAAQDGQSLKTRTMLQADINKLME 120
          GQAISNGNDALGILQTADKAMDEQLKILDITIKTKATQAAQDGQSLKTRTMLQADIN+LME
Sbjct: 62  GQAISNGNDALGILQTADKAMDEQLKILDITIKTKATQAAQDGQSLKTRTMLQADINRLME 121

Query: 121 ELDNIAINTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
          ELDNIAINTTSFNGKQLLSGNF NQEFQIGASSNQTVKATIGATQSSKIG+TRFETG +
Sbjct: 122 ELDNIAINTTSFNGKQLLSGNFINQEFQIGASSNQTVKATIGATQSSKIGLTRFETGGRIS 181

Query: 181 TSGVVGLTIKKNYNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVRATYDVKTGTV 240
          +SG V T+KNYNGI+DF+F VVISTSVGTGLGALA+EINK+ADKTGVRAT+ V+T G+
Sbjct: 182 SSGEVQFTLKNYNGIDDFQFQKVISTSVGTGLGALADEINKNADKTGVRATFTVETRGM 241

Query: 241 YAIKEGTTSDFAINGVTIGKIEYKDGNGSLISAINAVKDTTGVQASKDENGKLVLT 300
          A++ GTTS FAINGV IGK+ Y+DGD NG+L+SAIN+VKDTTGV+AS D NG+L+LTS
Sbjct: 242 AAVRAGTTSDTFAINGVKIGKVAYEDGDANGALVSAINSVKDTTGVVEASIDANGQLLLT 301

Query: 301 ADGRGIKITGDIGVSGILANQKENYGRSL-VKNDGRDINISGTNLSAIGMGTDDMISQ 359
          +GRGIKI G IG G+ I + ENYGR L +K +DI+ISGT LS G G ++ ISQ
Sbjct: 302 REGRIKIEGHIGGGAFINKDMIENYGRLLFWLKTTSKDISISGTGLSFTGFGASNFISQ 361

Query: 360 SSVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXX 419
          SVSLRESKGQ+ A ADAMGF S G SSI+ +M
Sbjct: 362 VSVSLRESKGQLDANTADAMGFSGVKNKG----LVLAASSIADYMSAEGSGFSAGSGYSVG 417

Query: 420 XXXKNLXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXXXQFAALKTTAANT---TDET 476
          K Y V QFA +KT+A N+ DET
Sbjct: 418 SGKGYSATLTANAIAISSASAISKIYNVSQSGSFSSGSTLSQFATMKTSAGNSLGAKDET 477

Query: 477 AGVTTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRD 536
          AGVTTLKGAMAVMDIAETAITNLDQIRADIGS+QNQVTSTINNITVTQVNVKAAESQIRD
Sbjct: 478 AGVTTLKGAMAVMDIAETAITNLDQIRADIGSVQNQVTSTINNITVTQVNVKAAESQIRD 537

Query: 537 VDFASESANYSKANILAQSGSYAMAQANSQQNVLRLLQ 575
          VDFA+ESANYSKANILAQSGSYAMAQANS QQNVLRLLQ
Sbjct: 538 VDFAAESANYSKANILAQSGSYAMAQANSVQQNVLRLLQ 576

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sp      P56964          Flagellin B [flaB] [Campylobacter jejuni] 571 AA
        FLB1_CAMJE
                                align

```

Score = 766 bits (1977), Expect = 0.0

Identities = 412/575 (71%), Positives = 459/575 (79%), Gaps = 4/575 (0%)

```

Query: 1  GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
          GFRINTN+ ALNA ANS +NA+ LD SLSRLSSGLRINSAADDASGMAIADSLRSQA TL
Sbjct: 1  GFRINTNIGALNAHANSVVNARELDKSLRLSSGLRINSAADDASGMAIADSLRSQAATL 60

Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDITIKTKATQAAQDGQSLKTRTMLQADINKLME 120
          GQAI+NGNDA+GILQTADKAMDEQLKILDITIKTKATQAAQDGQSLKTRTMLQADIN+LME
Sbjct: 61  GQAINNGNDAIGILQTADKAMDEQLKILDITIKTKATQAAQDGQSLKTRTMLQADINRLME 120

Query: 121 ELDNIAINTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
          ELDNIAINTTSFNGKQLLSGNF NQEFQIGASSNQ+KATIGATQSSKIG+TRFETG +
Sbjct: 121 ELDNIAINTTSFNGKQLLSGNFINQEFQIGASSNQTIKATIGATQSSKIGLTRFETGGRIS 180

Query: 181 TSGVVGLTIKKNYNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVRATYDVKTGTV 240

```



```

+SG V T+KNYNGI+DF+F VVISTSVGTGLGALAEIINKSADKTGVRAT+ V+T G+
Sbjct: 181 SSGEVQFTLKNYNGIDDFQFQKVISTSVGTGLGALAEIINKSADKTGVRATFTVETRGI 240

Query: 241 YAIKEGTTSDFAINGVTIGKIEYKDGNGSLISAINAVKDTTGVQASKDENGKLVLT 300
      A++ GTTS FAINGVTIG++ Y+DGDGNG+L++AIN+VKDTTGV+AS D NG+L+LTS
Sbjct: 241 AAVRAGTTSDTFAINGVTIGQVAYEDGDGNGALVAAINSVKDTTGVVEASIDANGQLLLTS 300

Query: 301 ADGRGIKITGDIGVSGILANQKENYGRSLVKN DGRDINISGTNLSAIGMGTTDMISQS 360
      +GRGIKI G+IG G+ I A+ KENYGRSLVKN D+DI ISG+NLS+ G G T ISQ+
Sbjct: 301 REGRGIKIDGNIGGGAFINADMKENYGRSLVKN DGDILISGSNLSSAGFGATQFISQA 360

Query: 361 SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXX 420
      SVSLRESKG+ A ADAMGF S K V SS+SA+M
Sbjct: 361 SVSLRESKGRFDANIADAMGFGS--ANKGVVLGGYSSVSAYMSSAGSGFSSGSGYSVGS 417

Query: 421 XKNLXXXXXXXXXXXXXXXXXNTYVXXXXXXXXXXXXXXXXXQFAALKTTAANTTDETAGVT 480
      KN Y V QFA +KTTA DETAGVT
Sbjct: 418 GKN-YSTGFANAIAISAASQLSTVYNVSAGSGFSSGSTLSQFATMKTTAFGVKDETAGVT 476

Query: 481 TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQNVKAAESQIRDVDFA 540
      TLKGAMAVMDIAETA TNLDQIRADIGS+QNQ+ TINNITVTQNVKAAES IRDVDFA
Sbjct: 477 TLKGAMAVMDIAETATTNLDQIRADIGSVQNQLQVTINNITVTQNVKAAESTIRDVDFA 536

Query: 541 SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
      +ESAN+SK NILAQSGSYAM+QAN+ QQNVL+LLQ
Sbjct: 537 AESANFSKYNILAQSGSYAMSQANAVQQNVLKLQ 571

```

tr Q6L5K6 **Flagellin (Fragment) [flaA] [Campylobacter lari]** 568 AA
align

Score = 766 bits (1977), Expect = 0.0

Identities = 407/575 (70%), Positives = 462/575 (79%), Gaps = 7/575 (1%)

```

Query: 1 GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
      GFRINTNVA+LNA+AN++LN+++LD SLSRLSSGLRINSAADDASGMAIADSLRSQA+TL
Sbjct: 1 GFRINTNVAASLNAQANANLNSRALDTSLSRLSSGLRINSAADDASGMAIADSLRSQASTL 60

Query: 61 GQAI SNNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
      GQAI+NGNDALGILQTADKAMDEQLKILDTIK KATQAAQDGQS KTR MLQADIN+LME
Sbjct: 61 GQAINNGNDALGILQTADKAMDEQLKILDTIKVKATQAAQDGQSTKTRNMLQADINRLME 120

Query: 121 ELDNIANTTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
      ELDNIANTTTSFNGKQLLSG FTNQEFQIG+ SNQ++KATIGATQSSKIGVTRFETG+ S
Sbjct: 121 ELDNIANTTTSFNGKQLLSGGFTNQEFQIGSQNSQSIKATIGATQSSKIGVTRFETGSMNS 180

Query: 181 TSGVVGLTIKKNYNGIEDFKFDNVVISTSVGTGLGALAEIINKSADKTGVRATYDVKTGTV 240
      TSG+ LTIKKNYNGI+DFKF VVISTSVGTG+GALAEIIN+ +D TGVRA + V+TTGV
Sbjct: 181 TSGIAQLTIKKNYNGIDDFKFQPVVISTSVGTGMGALAEIINRVSDVTGVRANFLVETGTV 240

Query: 241 YAIKEGTTSDFAINGVTIGKIEYKDGNGSLISAINAVKDTTGVQASKDENGKLVLT 300
      AIK TSQDF+INGV IG++EYKGDG NG+LISAIN+VKDTTGV+ASKD NG+LVL S
Sbjct: 241 GAIKADKTSQDFSINGVRIGEVEYKGDENGALISAINSVKDTTGVVEASKDANGRLVLNS 300

Query: 301 ADGRGIKITGDIGVSGILANQKENYGRSLVKN DGRDINISGTNLSAIGMGTTDMISQS 360
      DGRGIKI G +G+G+G+L ENYGRSLVKN D+DI ISGTNLS IGMG DMISQ+

```

```

Sbjct: 301 RDGRGIKIEGSMGMGAGVLKADYENYGRSLVKNDBGKDIAISGTNLSTIGMGAADMISQA 360
Query: 361 SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXXXX 420
      S+SLRESKG I      ADAMGFN+YKGGGK + T      SS+S FM
Sbjct: 361 SISLRESKGNIDTNVADAMGFNAYKGGGKMIVT--FSSVSTFMASENSGMSQSGYSVGS 418
Query: 421 XKNLXXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXXXXQFAALKTTAANTTDETAGVT 480
      KN+              +              F A      AA      D+ AGVT
Sbjct: 419 GKNMSLVYNSTEALAFVTAF---SIAFGTGASTGGASQFANFVASANIAAK--DQQAGVT 473
Query: 481 TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 540
      TLKGAMAVMDIAETAITNLDQIRAD+G++QNQ+T T+NNI+VTQVN+K+AES I RDVDFA
Sbjct: 474 TLKGAMAVMDIAETAITNLDQIRADLGAVQNQITRTLNNISVTQVNIKSAESNIRDVDFA 533
Query: 541 SESANYSKANILAQSGSYAMAQANSSQQNVRLRLQ 575
      +ESAN++K NILAQSGSYAM+QAN+ QQNV+RLLQ
Sbjct: 534 AESANFAKFNILAQSGSYAMSQANAVQQNVMRLQ 568

```

```

tr   Q6L5J8      Flagellin (Fragment) [flaA] [Campylobacter lari] 568 AA
                                align

```

Score = 765 bits (1975), Expect = 0.0

Identities = 407/575 (70%), Positives = 463/575 (79%), Gaps = 7/575 (1%)

```

Query: 1   GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
      GFRINTNVA+LNA+AN++LN+++LD SLSRLSSGLRINSAADDASGMAIADSLRSQA+TL
Sbjct: 1   GFRINTNVASLNAQANANLNSRALDTSLSRLSSGLRINSAADDASGMAIADSLRSQASTL 60
Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
      GQAI+NGNDALGILQTADKAMDEQLKILDTIK KATQAAQDGQS KTR MLQADIN+LME
Sbjct: 61  GQAINNGNDALGILQTADKAMDEQLKILDTIKVKATQAAQDGQSTKTRNMLQADINRLME 120
Query: 121 ELDNANIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
      ELDNANIANTT+FNGKQLLSG FTNQEFQIGA SNQ++KATIGATQSSKIGVTRFETG+ S
Sbjct: 121 ELDNANIANTTAFNGKQLLSGGFTNQEFQIGAQSNQSIKATIGATQSSKIGVTRFETGSMNS 180
Query: 181 TSGVVGLTIKKNYNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVRATYDVKTGTGV 240
      TSG+ LTIKKNYNGI+DFKF VVISTSVGTG+GALAEIN+ AD TGVRA + V+TTGV
Sbjct: 181 TSGIAQLTIKKNYNGIDDFKFQPVVISTSVGTGMGALAEINRVADVTGVRANFLVETGTGV 240
Query: 241 YAIKEGTTSQDFAINGVTIGKIEYKDGNGSLISAINAVKDTTGVQASKDENGKLVLTLS 300
      AIK TSQDF INGV IG++EYKDG NG+LISAIN+VKD'TTGV+ASKD NG+LVL S
Sbjct: 241 GAIKADKTSQDFTINGVRIGEVEYKDGDENGALISAINSVKDTTGVASKDANGRLVLNS 300
Query: 301 ADGRGIKITGDIGVSGILANQKENYGRSLVKNDBGKDINISGTNLISAIGMGTTDMISQS 360
      DGRGIKI G +G+G+G+L ENYGRSLVKNDBG+DI ISG+NLS IGMG DMISQ+
Sbjct: 301 RDGRGIKIEGSMGMGAGVLKADYENYGRSLVKNDBGKDIAISGSNLSTIGMGAGDMISQA 360
Query: 361 SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXXXX 420
      S+SLRESKG I      ADAMGFN+YKGGGK + T      SS+S+FM
Sbjct: 361 SISLRESKGNIDTNVADAMGFNAYKGGGKMIVT--FSSVSSFMNSEGSGMSQSGYSVGS 418
Query: 421 XKNLXXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXXXXQFAALKTTAANTTDETAGVT 480
      KN+              +              F A      AA      D+ AGVT
Sbjct: 419 GKNMSLVYNSTEALAFVTAF---SIAFGTGSSANGASQFANFVASANIAAK--DQQAGVT 473

```

Query: 481 TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 540
TLKGAMAVMDIAETAITNLDQIRAD+G++QNQ+T+T+NNI+VTQVN+K+AES IRDVDFA
Sbjct: 474 TLKGAMAVMDIAETAITNLDQIRADLGAVQNQITATLNNISVTQVNIKSAESNIRDVDFA 533

Query: 541 SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
+ESAN++K NILAQSGSYAM+QAN+ QQNV+RLLQ
Sbjct: 534 AESANFAKFNILAQSGSYAMSQANAVQQNVMRLLQ 568

tr Q9R951 Flagellin B [flaB] [Campylobacter jejuni] 572 AA
align

Score = 763 bits (1971), Expect = 0.0
Identities = 410/575 (71%), Positives = 459/575 (79%), Gaps = 4/575 (0%)

Query: 1 GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
GFRINTN+ +LN+ ANS +NA+ LD SLSRLSSGLRINSAADDASGMAIADSLRSQA TL
Sbjct: 2 GFRINTNIGSLNSHANSVVNARELDKSLRLSSGLRINSAADDASGMAIADSLRSQAATL 61

Query: 61 GQAIISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDQGQSLKTRTMLQADINKLME 120
GQAI+NGNDA+GILQTADKAMDEQLKILDTIKTKATQAAQDQGQSLKTRTMLQADIN+LME
Sbjct: 62 GQAINNGNDAIGILQTADKAMDEQLKILDTIKTKATQAAQDQGQSLKTRTMLQADINRLME 121

Query: 121 ELDNIANTTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
ELDNIANTTTSFNGKQLLSGNF NQEFQIGASSNQ+KATIGATQSSKIG+TRFETG +
Sbjct: 122 ELDNIANTTTSFNGKQLLSGNFINQEFQIGASSNQTIKATIGATQSSKIGLTRFETGGRIS 181

Query: 181 TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVRATYDVKTGTV 240
+SG V T+KNYNGI+DF+F VVISTSVGTGLGALAEINKSADKTGVRAT+ V+T G+
Sbjct: 182 SSGEVQFTLKNYNGIDDFQFQKVISTSVGTGLGALAEINKSADKTGVRATFTVETRGI 241

Query: 241 YAIKEGTTSDFAINGVTIGKIEYKDGNGSLISAINAVKDTTGVQASKDENGKLVLT 300
A++ GTTS FAINGVTIG++ Y+DGDGNG+L++AIN+VKDTTGV+AS D NG+L+LTS
Sbjct: 242 AAVRAGTTSDTFAINGVTIGQVAYEDGDNGALVAAINSVKDTTGVVEASIDANGQLLLTS 301

Query: 301 ADGRGIKITGDIGVSGILANQKENYGRSLSVKNDGRDINISGTNLSAIGMGTTDMISQS 360
+GRGIKI G+IG G+ I A+ KENYGRSLSVKNDG+DI ISG+NLS+ G G T ISQ+
Sbjct: 302 REGRGIKIDGNIGGGAFINADMKENYGRSLSVKNDGKDILISGSNLSSAGFGATQFISQA 361

Query: 361 SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXX 420
SVSLRESKG+ A ADAMGF S K V SS+SA+M
Sbjct: 362 SVSLRESKGRFDANIADAMGFGS--ANKGVVLGGYSSVSAYMSSAGSGFSSGSGYSVGS 418

Query: 421 XKNLXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXXXQFAALKTTAANTTDETAGVT 480
KN Y V QFA +KTTA DETAGVT
Sbjct: 419 GKN-YSTGFANAIAISAASQLSTVYNVSAGSGFSSGSTLSQFATMKTTFAGVKDETAGVT 477

Query: 481 TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 540
TLKGAMAVMDIAETA TNLDQIRADIGS+QNQ+ TINNITVTQVNVKAAES IRDVDFA
Sbjct: 478 TLKGAMAVMDIAETATTNLDQIRADIGSVQNQLQVTINNITVTQVNVKAAESTIRDVDFA 537

Query: 541 SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
+ESAN+SK NILAQSGSYAM+QAN+ QQNV+LLQ
Sbjct: 538 AESANFSKYNILAQSGSYAMSQANAVQQNVLKLLQ 572

tr Q933V4 **Flagellin A (Fragment) [flaA] [Campylobacter jejuni]** 554 AA
align

Score = 762 bits (1968), Expect = 0.0

Identities = 411/558 (73%), Positives = 447/558 (79%), Gaps = 4/558 (0%)

```

Query: 10  ALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLGQAISNGND 69
          ALNAKAN+DLN+KSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLGQAISNGND
Sbjct: 1   ALNAKANADLNSKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLGQAISNGND 60

Query: 70  ALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLMEELDNIANTT 129
          ALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LMEELDNIANTT
Sbjct: 61  ALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLMEELDNIANTT 120

Query: 130 SFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSFTSGVVGLTI 189
          SFNGKQLLSGNF NQEFQIGASSNQTVKATIGATQSSKIG+TRFETG + +SG V T+
Sbjct: 121 SFNGKQLLSGNFINQEFQIGASSNQTVKATIGATQSSKIGLTRFETGGRISSSGEVQFTL 180

Query: 190 KNYNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVRATYDVKTGTVYAIKEGTTS 249
          KNYNGI+DF+F VVISTSVGTGLGALA+EINK+ADKTGVRAT+ V+T G+ A++ GTTS
Sbjct: 181 KNYNGIDDFQFQKVISTSVGTGLGALADEINKNADKTGVRATFTVETRGMMAVRAGTTS 240

Query: 250 QDFAINGVTIGKIEYKDGNGSLISAINAVKDTTGVQASKDENGKLVLTADGRGIKIT 309
          DF INGV IGK+EYKDG NG+L++AIN+VKDTTGV+AS D NG+L+L+S +GRGIKI
Sbjct: 241 DDFTINGVKIGKVEYKDGANGALVAAINSVKDTTGVVEASIDANGQLLLSSREGRGIKIE 300

Query: 310 GDIGVGSGILANQKENYGRSLSVKNDGRDINISGTNLSAIGMGTTDMISQSSVSLRESKG 369
          G IG G+ I N ENYGRSLSVKNDG+DI +SGT LS G G ISQ+SVSLRESKG
Sbjct: 301 GSIGRGAFINPNMMENYGRSLSVKNDGKDILVSGTGLSFAGFGANSFISQASVSLRESKG 360

Query: 370 QISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXXXXKNLXXXXX 429
          Q+ A ADAMGF S G V SS+SA+M KN
Sbjct: 361 QLDANTADAMGFGSVNKG---VMLAGYSSVSAYMSSAGSGFSSGSGYSVSGSKNYSTGFA 417

Query: 430 XXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXXXQFAALKTTAANTTDETAGVTTLKGAMAVM 489
          Y V QFA +KTTA DETAGVTTLKGAMAVM
Sbjct: 418 NAIISAASQLSA-VYNVSAGSGFSSQSGLSQFATMKTTAFGVKDETAGVTTLKGAMAVM 476

Query: 490 DIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFAESANYSKA 549
          DIAETAITNLDQIRADIGS+QNQVTSTINNITVTQVNVKAAESQIRDVDFA+ESANYSKA
Sbjct: 477 DIAETAITNLDQIRADIGSVQNQVTSTINNITVTQVNVKAAESQIRDVDFAAESANYSKA 536

Query: 550 NILAQSGSYAMAQANSSQ 567
          NILAQSGSYAMAQANS Q
Sbjct: 537 NILAQSGSYAMAQANSVQ 554

```

tr Q6L5K1 **Flagellin (Fragment) [flaA] [Campylobacter lari]** 568 AA
align

Score = 762 bits (1967), Expect = 0.0

Identities = 404/575 (70%), Positives = 463/575 (80%), Gaps = 7/575 (1%)

```

Query: 1   GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
          GFRINTNVA+LNA+AN++LN+++LD SLRLSSGLRINSAADDASGMAIADSLRSQA+TL

```

```

Sbjct: 1   GFRINTNVASLNAQANANLNSRALDTSLSRLSSGLRINSAADDASGMAIADSLRSQASTL 60

Query: 61   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
           GQAI+NGNDALGILQTADKAMDEQLKILDTIK KATQAAQDGQS KTR MLQADIN+LME

Sbjct: 61   GQAINNGNDALGILQTADKAMDEQLKILDTIKVKATQAAQDGQSTKTRNMLQADINRLME 120

Query: 121  ELDNIAINTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
           ELDNIAINTT+FNGKQLLSG FTNQEFQIG+ SNQ++KATIGATQSSKIGVTRFETG+ S

Sbjct: 121  ELDNIAINTTAFNGKQLLSGGFTNQEFQIGSQSNQSIKATIGATQSSKIGVTRFETGSMK 180

Query: 181  TSGVVGLTIKKNYNGIEDFKFDNVVISTSVGTGLGALAEIINKSADKTGVRATYDVKTGTG 240
           SG+ LTIKKNYNGI+DFKF VVISTSVGTG+GALAEIIN+ AD TGVRA + V+TTGV

Sbjct: 181  DSGIAQLTIKKNYNGIDDFKFQPVVISTSVGTGMGALAEINRVADVTGVRANFLVETGTG 240

Query: 241  YAIKEGTTSQDFAINGVTIGKIEYKDGNGSLISAINAVKDTTGVQASKDENGKLVLT 300
           AIK TSQDF+INGV IG++EYKDG NG+LISAIN+VKDTTGV+ASKD NG+LVL S

Sbjct: 241  GAIKADKTSQDFSINGVRIGEVEYKDGDENGALISAINSVKDTTGVASKDANGRLVLNS 300

Query: 301  ADGRGIKITGDIGVSGILANQKENYGRSLSVKNDGRDINISGTNLSAIGMGTTDMISQS 360
           DGRGIKI G +G+G+G+L ENYGRSLSVKNDG+DI ISG+NLS IGMG T MISQ+

Sbjct: 301  RDGRGIKIEGSMGMGAGVLKADYENYGRSLSVKNDGKDIAISGSNLSTIGMGATQMISQA 360

Query: 361  SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXX 420
           S+SLRESKG I ADAMGFN+YKGGGK + T SS+S+FM

Sbjct: 361  SISLRESKGNIDTNVADAMGFNAYKGGGKMIVT--FSSVSSFMDSSSGMSAGSGYSVGS 418

Query: 421  XKNLXXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXXXQFAALKTTAANTTDETAGVT 480
           KN+ + F + AA D+ AGVT

Sbjct: 419  GKNMSLVYNSTEALAFVTAF---SIAFGTGASTGWSSQSANFVTSASIAAK--DQQAGVT 473

Query: 481  TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 540
           TLKGAMAVMDIAETAITNLDQIRAD+G++QNQ+T+T+NNI+VTQVN+K+AES IRDVDFA

Sbjct: 474  TLKGAMAVMDIAETAITNLDQIRADLGAVQNQITATLNNISVTQVNIKSAESNIRDVDFA 533

Query: 541  SESANYSKANILAQSGSYAMAQANSSQQNVRLRLQ 575
           +ESAN++K NILAQSGSYAM+QAN+ QQNV+RLRLQ

Sbjct: 534  AESANFAKFNILAQSGSYAMSQANAVQQNVMRLLQ 568

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```

tr   Q9R954      Flagellin B [flaB] [Campylobacter jejuni]      572 AA
                                align

```

Score = 761 bits (1966), Expect = 0.0

Identities = 410/575 (71%), Positives = 457/575 (79%), Gaps = 4/575 (0%)

```

Query: 1   GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
           GFRINTN+ LNA ANS +NA+ LD SLSRLSSGLRINSAADDASGMAIADSLRSQA TL

Sbjct: 2   GFRINTNIGPLNAHANSVVNARELDKSLRLSSGLRINSAADDASGMAIADSLRSQAATL 61

Query: 61   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
           GQAI+NGNDA+GILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LME

Sbjct: 62   GQAINNGNDAIGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 121

Query: 121  ELDNIAINTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
           ELDNIAINTTSFNGKQLLSGNF NQEFQIGASSNQ+KATIGATQSSKIG+TRFETG +

Sbjct: 122  ELDNIAINTTSFNGKQLLSGNFINQEFQIGASSNQTIKATIGATQSSKIGLTRFETGGRIS 181

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Query: 181 TSGVVGLTIKNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVRATYDVKTTGV 240
      +SG V T+KNYNGI+DF+F VVISTSVGTGLGALAEINKSADKTGVRAT+ V+T G+
Sbjct: 182 SSGEVQFTLKNYNGIDDFQFQKVISTSVGTGLGALAEINKSADKTGVRATFTVETRGI 241

Query: 241 YAIKEGTTSDFAINGVTIGKIEYKDGNGSLISAINAVKDTTGVQASKDENGKLVLT 300
      A++ GTTS FAINGVTIG++ Y+DGDGNG+L++AIN+VKD'TTGV+AS D NG+L+LTS
Sbjct: 242 AAVRAGTTSDTFAINGVTIGQVAYEDGDGNGALVAAINSVKD'TTGVEASIDANGQLLLTS 301

Query: 301 ADGRGIKITGDIGVSGILANQKENYGRSLVKN DGRDINISGTNLSAIGMGTTDMISQS 360
      +GRGIKI G+IG G+ I A+ KENYGRSLVKN DG+DI ISG+NLS+ G G T ISQ+
Sbjct: 302 REGRGIKIDGNIGGGAFINADMKENYGRSLVKN DGDILISGSNLSSAGFGATQFISQA 361

Query: 361 SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXX 420
      SVSLRESKG+ A ADAMGF S K V SS+SA+M
Sbjct: 362 SVSLRESKGRFDANIADAMGFGS---ANKGVVLGGYSSVSAYMSSAGSGFSSSGYSVGS 418

Query: 421 XKNLXXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXXXQFAALKTTAANTTDETAGVT 480
      KN Y V QFA +KTTA DETAGVT
Sbjct: 419 GKN-YSTGFANAIAISAASQLSTVYNVSAGSGFSSGSTLSQFATMKTTAFGVKDETAGVT 477

Query: 481 TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 540
      TLKGAMAVMDIAET TNLDQIRADIGS+QNQ+ TINNITVTQVNVKAAES IRDVDFA
Sbjct: 478 TLKGAMAVMDIAETD'TTNLDQIRADIGSVQNQLQVTINNITVTQVNVKAAESTIRDVDFA 537

Query: 541 SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
      +ESAN+SK NILAQSGSYAM+QAN+ QQNVL+LLQ
Sbjct: 538 AESANFSKYNILAQSGSYAMSQANAVQQNVLKLLQ 572

```

```

tr Q6L5J9 Flagellin (Fragment) [flaA] [Campylobacter lari] 568 AA
      align

```

Score = 761 bits (1965), Expect = 0.0

Identities = 405/575 (70%), Positives = 462/575 (79%), Gaps = 7/575 (1%)

```

Query: 1 GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
      GFRINTNVA+LNA+AN++LN+++LD SLRLSSGLRINSAADDASGMAIADSLRSQA+TL
Sbjct: 1 GFRINTNVASLNAQANANLNSRALD'TSLRLSSGLRINSAADDASGMAIADSLRSQASTL 60

Query: 61 GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
      GQAI+NGNDALGILQTADKAMDEQLKILDTIK KATQAAQDGQS KTR MLQADIN+LME
Sbjct: 61 GQAINNGNDALGILQTADKAMDEQLKILDTIKVKATQAAQDGQSTKTRNMLQADINRLME 120

Query: 121 ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
      ELDNIANTT+FNGKQLLSG FTNQEFQIGA SNQ++KATIGATQSSKIGVTRFETG+ S
Sbjct: 121 ELDNIANTTAFNGKQLLSGGFTNQEFQIGAQSNQSIKATIGATQSSKIGVTRFETGSMNS 180

Query: 181 TSGVVGLTIKNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVRATYDVKTTGV 240
      SG+ LTIKNGYNGI+DFKF VVISTSVGTG+GALAEIN+ AD TGVRA + V+TTGV
Sbjct: 181 DSGIAQLTIKNGYNGIDDFKFQPVVISTSVGTGMGALAEINRVADVTGVRANFLVETTV 240

Query: 241 YAIKEGTTSDFAINGVTIGKIEYKDGNGSLISAINAVKDTTGVQASKDENGKLVLT 300
      AIK TSQ+F INGV IG++EYKDG NG+LISAIN+VKD'TTGV+ASKD NG+LVL S
Sbjct: 241 GAIKADKTSQNFTINGVRIGEVEYKDGDENGALISAINSVKD'TTGVEASKDANGRLVLNS 300

```

```

Query: 301 ADGRGIKITGDIGVSGILANQKENYGRSLVKNDGRDINISGTNLSAIGMGTTDMISQS 360
          DGRGIKI G +G+G+G+L      ENYGRSLVKNDG+DI ISG+NLS IGMG T MISQ+
Sbjct: 301 RDGRGIKIEGSMGMGAGVLKADYENYGRSLVKNDGKDILISGNSLSTIGMGATQMISQA 360

Query: 361 SVSLRESKQGISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXX 420
          S+SLRESKG I      ADAMGFN+YKGGGK + T      SS+S+FM
Sbjct: 361 SISLRESKGNIDTNVADAMGFNAYKGGGKMIVT--FSSVSSFMASSGSGMSESGYSVNS 418

Query: 421 XKNLXXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXXXQFAALKTTAANTTDETAGVT 480
          KN+              +              F A      AA      D+ AGVT
Sbjct: 419 GKNMSLVYNSTEALAFVTAF---SIAFGTGSSANGRSQFANFVASANIAAK--DQQAGVT 473

Query: 481 TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 540
          TLKGAMAVMDIAETAITNLDQIRAD+G++QNQ+T+T+NNI+VTQVN+K+AES I RDVDFA
Sbjct: 474 TLKGAMAVMDIAETAITNLDQIRADLGAVQNQITATLNNISVTQVNIKSAESNIRDVDFA 533

Query: 541 SESANYSKANILAQSGSYAMAQANSSQQNVRLRLQ 575
          +ESAN++K NILAQSGSYAM+QAN+ QQNV+RLLQ
Sbjct: 534 AESANFAKFNILAQSGSYAMSQANAVQQNVMRLLQ 568

```

```

tr   Q93NL8      Flagellin A (Fragment) [flaA] [Campylobacter jejuni] 558 AA
                                align

```

Score = 760 bits (1963), Expect = 0.0

Identities = 410/561 (73%), Positives = 451/561 (80%), Gaps = 6/561 (1%)

```

Query: 10  ALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLGQAISNGND 69
          ALNAKAN+DLN+KSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLGQAISNGND
Sbjct: 1   ALNAKANADLNSKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLGQAISNGND 60

Query: 70  ALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLMEELDNIAINTT 129
          ALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LMEELDNIAINTT
Sbjct: 61  ALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLMEELDNIAINTT 120

Query: 130 SFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSFTSGVVGLTI 189
          SFNGKQLLSGNF NQEFQIGASSNQT+KATIGATQSSKIG+TRFETG + +SG V  T+
Sbjct: 121 SFNGKQLLSGNFINQEFQIGASSNQTIKATIGATQSSKIGLTRFETGGRISSSGEVQFTL 180

Query: 190 KNYNGIEDFKFDNVVISTSVGTGLGALAEIEINKSADKTGVRATYDVKTGTGVYAIKEGTTS 249
          KNYNGI+DFKF VVISTSVGTGLGALA+EINK+ADKTGVRAT+ V+T G+ A++ GTTS
Sbjct: 181 KNYNGIDDFKFQKVISTSVGTGLGALADEINKNADKTGVRATFTVETRGMMAVRAGTTS 240

Query: 250 QDFAINGVTIGKIEYKDGNGSLISAINAVKDTTGVQASKDENGKLVLTSAADGRGIKIT 309
          DFAINGV IGK++YKGDG NG+L+SAIN+VKD'TTGV+AS D NG+L+L+S +GRGIKI
Sbjct: 241 DDFAINGVKIGKVDYKGDGANGALVSAINSVKDTTGVVEASIDANGQLLLSSREGRGIKIE 300

Query: 310 GDIGVSGILANQKENYGRSLVKNDGRDINISGTNLSAIGMGTTDMISQSSVSLRESKG 369
          G+IG G+ I + KENYGRSLVKNDG+DI ISG +LS+ G GTT ISQ+SVSLRESKG
Sbjct: 301 GNIGGGAFINTDMKENYGRSLVKNDGKDILISGNSLSSAGFGTTQFISQASVSLRESKG 360

Query: 370 QISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXXXXKNLXXXXX 429
          QI A ADAMGF S G V      SS+SA+M      KN
Sbjct: 361 QIDANIADAMGFGSVNKG---VVLGGYSSVSAYMSAEGSGFSAGSGYSVGSTKNYSATLS 417

Query: 430 XXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXXXQFAALKTTAANTTD---ETAGVTTTLKGAM 486

```

```

          Y V                      QFA +KT+  N+      ETAGVTTLKGAM
Sbjct: 418 ANTITISAASQLSKVYNVSAGSGFSSQSGLSQFATMKTSVGNLSGVKAETAGVTTLKGAM 477

Query: 487 AVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFASESANY 546
          AVMDIAETAITNLDQIRADIGS+QNQ+  TINNITVTQVNVKAAESQIRDVDF+ESANY
Sbjct: 478 AVMDIAETAITNLDQIRADIGSVQNQLQVTINNITVTQVNVKAAESQIRDVDFAAESANY 537

Query: 547 SKANILAQSGSYAMAQANSSQ 567
          SKANILAQSGSYAMAQANS  Q
Sbjct: 538 SKANILAQSGSYAMAQANSVQ 558

```

```

tr   Q93NL7          Flagellin A (Fragment) [flaA] [Campylobacter jejuni] 556 AA
                                align

```

Score = 756 bits (1953), Expect = 0.0
 Identities = 409/560 (73%), Positives = 450/560 (80%), Gaps = 6/560 (1%)

```

Query: 10  ALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLGQAIISNGND 69
          ALNAKAN+DLN+KSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLGQAIISNGND
Sbjct: 1   ALNAKANADLNSKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLGQAIISNGND 60

Query: 70  ALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLMEELDNIANTT 129
          ALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LMEELDNIANTT
Sbjct: 61  ALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLMEELDNIANTT 120

Query: 130 SFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSFTSGVVGLTI 189
          SFNGKQLLSGNF NQEFQIGASSNQ+KATIGATQSSKIG+TRFETG + +SG V  T+
Sbjct: 121 SFNGKQLLSGNFINQEFQIGASSNQTIKATIGATQSSKIGLTRFETGGRISSSGEVQFTL 180

Query: 190 KNYNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVRATYDVKTGTVYAIKEGTTS 249
          KNYNGI+DFKF  VVISTSVGTGLGALA+EINK+ADKTGVRAT+ V+T G+ A++ GTTS
Sbjct: 181 KNYNGIDDFKFQKVISTSVGTGLGALADEINKNADKTGVRATFTVETRGMMAVRAGTTS 240

Query: 250 QDFAINGVTIGKIEYKDGNGSLISAINAVKDDTTGVQASKDENGKLVLTSDAGRGIKIT 309
          DFAIN V IGK++YKGDG NG+L++AIN+VKDDTTGV+AS D NG+L+LTS +GRGIKI
Sbjct: 241 DDFAINEVKIGKVDYKGDANGALVAAINSVKDDTTGVEASIDANGQLLLTSREGRGIKID 300

Query: 310 GDIGVGSGILANQKENYGRSLSLVKNDGRDINISGTNLSAIGMGTTDMISQSSVSLRESKG 369
          G+IG G+ I  + KENYGRSLSLVKNDG+DI ISG +LS+ G GTT ISQ+SVSLRESKG
Sbjct: 301 GNIGGGAFINTDMKENYGRSLSLVKNDGKDILISGNSLSSAGFGTTQFISQASVSLRESKG 360

Query: 370 QISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXXXXKNLXXXXX 429
          QI A  ADAMGF S  G          SS+SA+M          KN
Sbjct: 361 QIDANIADAMGFGSVNKG----VVLGYSSVSAYMSAEGSGFSAGSGYSVGSTKNYSTVLT 416

Query: 430 XXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXXXXQFAALKTTAA--NTTDETAGVTTLKGAMA 487
          Y V                      QFA +K +A  +      ETAGVTTLKGAMA
Sbjct: 417 ANAITISAASQLSKVYNVSAGSGFSSGSNLSQFATMKISAGAFDVKAEATAGVTTLKGAMA 476

Query: 488 VMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFASESANY 547
          VMDIAETAITNLDQIRADIGS+QNQVTSTINNITVTQVNVKAAESQIRDVDF+ESANY
Sbjct: 477 VMDIAETAITNLDQIRADIGSVQNQVTSTINNITVTQVNVKAAESQIRDVDFAAESANY 536

Query: 548 KANILAQSGSYAMAQANSSQ 567
          KA+ILAQSGSYAMAQANS  Q

```


Sbjct: 537 KAHILAQSGSYAMAQANSVQ 556

tr Q6L5K5 **Flagellin (Fragment) [flaA] [Campylobacter lari]** 566 AA
align

Score = 756 bits (1952), Expect = 0.0

Identities = 404/576 (70%), Positives = 466/576 (80%), Gaps = 11/576 (1%)

Query: 1 GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
 GFRINTNVA+LNA+ N++LN+++LD+SLSRLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 1 GFRINTNVASLNAQNNANLNSRALDSSLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60

Query: 61 GQAISNGNDALGILQTADKAMDEQLKILDITIKTKATQAAQDGQSLKTRTMLQADINKLME 120
 GQAI+NGNDALGILQTADKAMDEQLKILDITIK KATQAAQDGQS KTR MLQADIN+LME
Sbjct: 61 GQAINNGNDALGILQTADKAMDEQLKILDITIKVKATQAAQDGQSTKTRNMLQADINRLME 120

Query: 121 ELDNINANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
 ELDNIANTT+FNGKQLL G FTNQ FQIGA SNQT++A+IGATQSSKIGVTRFETG+ S
Sbjct: 121 ELDNIANTTAFNGKQLLGGGFTNQSFQIGAQSNQTIQASIGATQSSKIGVTRFETGSM 180

Query: 181 TSGVVGLTIKKNYNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVRATYDVKTGTG 240
 +SGV LTIKKNYNGI+DFKF VVIS+SVGTG+GALAEIN+ +D TGVRA + V+TTG
Sbjct: 181 SSGVAQLTIKKNYNGIDDFKFQPVVIVSSVGTGMGALAEINRVSDITGVRANFLVQTTGA 240

Query: 241 YAIKEGTTSQDFAINGVTIGKIEYKDGNGSLISAINAVKDTTGVQASKDENGKLVLS 300
 +IK TSQDF INGV IG++EYKDG NG+LISAIN+VKDTTGV+ASKD NG+LVL S
Sbjct: 241 GSIKADKTSQDFTINGVRIGEVEYKDGDENGALISAINSVKDTTGVASKDANGRLVLNS 300

Query: 301 ADGRGIKITGDIGVSGILANQKENYGRSLSVKNDGRDINISGTNLSAIGMGTTDMISQS 360
 DGRGI+ITG +G G+GIL + +N+GRSLSVKNDG+DI ISG+NLSAIGMGTTDMISQ+
Sbjct: 301 RDGRGIEITGSMGPGAGILKDDYKNFGRLSLVKNDGKDILISGSNLSAIGMGTTADMISQA 360

Query: 361 SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXX 420
 S+SLRESKG I ADAMGFN+YKGGGK V T ++ISAFM
Sbjct: 361 SISLRESKGNIDTHVADAMGFNAYKGGGKMVVT--FATISAFMSSAGSGMSAGSGYSVGS 418

Query: 421 XKNLXXXXXXXXXXXXXXXXXNTYVXXXXXXXXXXXXXXXXXQFAALKTTA-ANTTDETAGV 479
 K++ T QFAA T+A D+ AGV
Sbjct: 419 GKDMSALYEGNLAFV-----TAFSVAFGFSKNDGTSQFAAFATSANIAAKDQQAGV 470

Query: 480 TTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDF 539
 TTLKGAMAVMDIAETAITNLDQIRAD+G++QNQ+T+T+NNI+VTQVN+K+AES IRDVDF
Sbjct: 471 TTLKGAMAVMDIAETAITNLDQIRADLGAVQNQITATLNNISVTQVNIKSAESNIRDVDF 530

Query: 540 ASESANYSKANILAQSGSYAMAQANSQQNVRLRLQ 575
 A+ESAN++K NILAQSGSYAM+QAN+ QQNV+RLLQ
Sbjct: 531 AAESANFAKFNILAQSGSYAMSQANAVQQNVRLRLQ 566

tr Q6L5K8 **Flagellin (Fragment) [flaA] [Campylobacter lari]** 567 AA
align

Score = 755 bits (1950), Expect = 0.0

Identities = 406/576 (70%), Positives = 463/576 (79%), Gaps = 10/576 (1%)

```

Query: 1   GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
          GFRINTNVA+LNA+ N++LN+++LD+SLSRLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 1   GFRINTNVASLNAQNNANLNSRALDSSLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60

Query: 61  GQAIISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
          GQAI+NGNDALGILQTADKAMDEQLKILDTIK KATQAAQDGQS KTR MLQADIN+LME
Sbjct: 61  GQAINNGNDALGILQTADKAMDEQLKILDTIKVKATQAAQDGQSTKTRNMLQADINRLME 120

Query: 121 ELDNIAINTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
          ELDNIAINTT+FNGKQLLSG FTNQ FQIGA SNQT++A+IGATQSSKIGVTRFETG+ S
Sbjct: 121 ELDNIAINTTAFNGKQLLSGGFTNQSFQIGAQSNQTIQASIGATQSSKIGVTRFETGSMH 180

Query: 181 TSGVVGLTIKKNYNGIEDFKFDNVVISTSVGTGLGALAEIINKSADKTGVRATYDVKTGGV 240
          +SGV LTIKKNYNGI+DFKF VVIS+SVGTG+GALAEIIN+ AD TGVRA + V+TTG
Sbjct: 181 SSGVAQLTIKKNYNGIDDFKFQPVVIVSSSVGTGMGALAEIINRVADVTGVRANFLVQTTGA 240

Query: 241 YAIKEGTTSQDFAINGVTIGKIEYKDGNGSLISAINAVKDDTTGVQASKDENGKLVLT 300
          +IK TSQDF INGV IG++EYKDG NG+LISAIN+VKDDTTGV+ASKD NG+LVL S
Sbjct: 241 GSIKADKTSQDFTINGVKIGEVEYKDGDENGALISAINSVKDDTTGVEASKDANGRLVLNS 300

Query: 301 ADGRGIKITGDIGVSGILANQKENYGRSLVKN DGRDINISGTNLSAIGMGTTDMISQS 360
          DGRGI+ITG++GVGSG+L + +N+GRSLVKN DG+DI ISG+ LS IGMG DMISQ+
Sbjct: 301 RDGRGIEITGNMGVSGSVLKKDYKNFGRSLVKN DGDILISGGLSFIGMGAGDMISQA 360

Query: 361 SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXX 420
          SVSLRESKG I ADAMGFN+YKGGGK V T SSI AFM
Sbjct: 361 SVSLRESKGNIDTHVADAMGFNAYKGGGKMVIT--FSSIEAFMSSNGSGMSAGSGFSIGS 418

Query: 421 XKNLXXXXXXXXXXXXXXXXXXXXNTYVVVXXXXXXXXXXXXXXXXXQFAALKTTAA-NTTDETAGV 479
          K + T QFAA TA+ D+ AGV
Sbjct: 419 GKEMSKIYNSGNLALV-----TVFSNAFGFSAKNDGSSQFAAFAGTASIAAKDQQAGV 471

Query: 480 TTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDF 539
          TTLKGAMAVMDIAETAITNLDQIRAD+G++QNQ+T T+NNI+VTQVN+K+AES IRDVDF
Sbjct: 472 TTLKGAMAVMDIAETAITNLDQIRADLGAVQNQITRTLNNISVTQVNIKSAESNIRDVDF 531

Query: 540 ASESANYSKANILAQSGSYAMAQANSSQQNVRLRLQ 575
          A+ESAN++K NILAQSGSYAM+QAN+ QQNV+RLRLQ
Sbjct: 532 AAESANFAKFNILAQSGSYAMSQANAVQQNVRLRLQ 567

```

```

tr   Q6L5J7      Flagellin (Fragment) [flaA] [Campylobacter lari] 571 AA
                                align

```

Score = 755 bits (1950), Expect = 0.0

Identities = 406/580 (70%), Positives = 464/580 (80%), Gaps = 14/580 (2%)

```

Query: 1   GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
          GFRINTNVA+LNA+ N++LN+++LD+SLSRLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 1   GFRINTNVASLNAQNNANLNSRALDSSLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60

Query: 61  GQAIISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
          GQAI+NGN ALGILQTADKAMDEQLKILDTIK KATQAAQDGQS KTR MLQADIN+LME
Sbjct: 61  GQAINNGALGILQTADKAMDEQLKILDTIKVKATQAAQDGQSTKTRNMLQADINRLME 120

```

```

Query: 121 ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
          ELDNIANTT+FNGKQLLSG FTNQ FQIGA SNQT++A+IGATQSSKIGVTRFETG+ S
Sbjct: 121 ELDNIANTTAFNGKQLLSGGFTNQSFQIGAQSNQTIQASIGATQSSKIGVTRFETGSMH 180

Query: 181 TSGVVGLTIKKNYNGIEDFKFDNVVISTSVGTGLGALAEIINKSADKTGVRATYDVKTGTG 240
          TSGV LTIKKNYNGI+DFKF VVIS+SVGTG+GALAEIIN+ AD TGVRA + V+TTG
Sbjct: 181 TSGVAQLTIKKNYNGIDDFKFQPVVSSSVGTGMGALAEIINRVADVTGVRANFLVQTTGA 240

Query: 241 YAIKEGTTSDFAINGVTIGKIEYKDGNGSLISAINAVKDDTTGVQASKDENGKLVLT 300
          +IK TSQDF INGV IG++EYKDG NG+LISAIN+VKDDTTGV+ASKD NG+LVL S
Sbjct: 241 GSIKADKTSQDFTINGVKIGEVEYKDGDENGALISAINSVKDDTTGVEASKDANGRLVLNS 300

Query: 301 ADGRGIKITGDIGVSGILANQKENYGRSLVKNDDGRDINISGTNLSAIGMGTDMISQS 360
          DGRGI+ITG++GVGSG+L + +N+GRSLVKNDDG+DI ISG+ LS IGMG DMISQ+
Sbjct: 301 RDGRGIEITGNMGVSGVLKDDYKNFGRSLVKNDDGKDILISGSLSFIMGAGDMISQA 360

Query: 361 SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXX 420
          S+SLRESKG I ADAMGFN+YKGGGK V T SSI AFM
Sbjct: 361 SISLRESKGNIDTHIADAMGFNAYKGGGKMVVT--FSSIEAFMSSDGSMSAGSGFSIGS 418

Query: 421 XKNLXXXXXXXXXXXXXXXXXXXXNTYVXXXXXXXXXXXXXQFAALKTTAANTT-----DE 475
          K + T QFAA +A N + D+
Sbjct: 419 GKEMSKIYNSGNLALV-----TAFSNAFGFSAKGDGASQFAAFAISAGNNSQIAAKDQ 471

Query: 476 TAGVTTTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIR 535
          AGVTTTLKGAMAVMDIAETAITNLDQIRADIG++QNQ+T+T+NNI+VTQVN+K+AES IR
Sbjct: 472 QAGVTTTLKGAMAVMDIAETAITNLDQIRADIGAVQNQITATLNNISVTQVNIKSAESNIR 531

Query: 536 DVDFASESANYSKANILAQSGSYAMAQANSSQQNVRLRLQ 575
          DVDF+ESAN++K NILAQSGSYAM+QAN+ QQNV+RLLQ
Sbjct: 532 DVDFAAESANFAKFNILAQSGSYAMSQANAVQQNVRLRLQ 571

```

tr Q6L5K2 Flagellin (Fragment) [flaA] [Campylobacter lari] 567 AA
align

Score = 754 bits (1948), Expect = 0.0
Identities = 405/576 (70%), Positives = 463/576 (80%), Gaps = 10/576 (1%)

```

Query: 1 GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
          GFRINTNVA+LNA+ N++LN+++LD+SLSRLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 1 GFRINTNVASLNAQNNANLNSRALDSSLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60

Query: 61 GQAISNGNDALGILQTADKAMDEQLKILDITIKTKATQAAQDGQSLKTRTMLQADINKLME 120
          GQAI+NGNDALGILQTADKAMDEQLKILDITIK KATQAAQDGQS KTR MLQADIN+LME
Sbjct: 61 GQAINNGNDALGILQTADKAMDEQLKILDITIKVKATQAAQDGQSTKTRNMLQADINRLME 120

Query: 121 ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
          ELDNIANTT+FNGKQLLSG FTNQ FQIGA SNQT++A+IGATQSSKIGVTRFETG+ S
Sbjct: 121 ELDNIANTTAFNGKQLLSGGFTNQSFQIGAQSNQTIQASIGATQSSKIGVTRFETGSMH 180

Query: 181 TSGVVGLTIKKNYNGIEDFKFDNVVISTSVGTGLGALAEIINKSADKTGVRATYDVKTGTG 240
          +SGV LTIKKNYNGI+DFKF VVIS+SVGTG+GALAEIIN+ AD TGVRA + V+TTG
Sbjct: 181 SSGVAQLTIKKNYNGIDDFKFQPVVSSSVGTGMGALAEIINRVADVTGVRANFLVQTTGA 240

Query: 241 YAIKEGTTSDFAINGVTIGKIEYKDGNGSLISAINAVKDDTTGVQASKDENGKLVLT 300

```

```

      +IK   TSQDF INGV IG++EYKGDG NG+LISAIN+VKD TTGV+ASKD NG+LVL S
Sbjct: 241 GSIKADKTSQDFTINGVKIGEVEYKGDENGALISAINSVKDTTGVEASKDANGRLVLNS 300

Query: 301 ADGRGIKITGDIGVGSgilANQKENYGRSLVKNdGRDINISGTNLSAIGMGTTDMISQS 360
      DGRGI+ITG++GVGSG+L + +N+GRSLVKNdG+DI ISG+ LS IGMG DMISQ+
Sbjct: 301 RDGRGIEITGNMGVGSgVLKDDYKNFGRSLVKNdGKDILISGSGLSFIGMGAGDMISQA 360

Query: 361 SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXX 420
      S+SLRESKG I ADAMGFN+YKGGGK V T SSI AFM
Sbjct: 361 SISLRESKGNIDTHIADAMGFNAYKGGGKMVVT--FSSIEAFMSSDGSMSAGSGFSIGS 418

Query: 421 XKNLXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXXXQFAALKTTAA-NTTDETAGV 479
      K + T QFAA TA+ D+ AGV
Sbjct: 419 GKEMSKIYNSGNLALV-----TVFSNAFGFSAKNDGSSQFAAFAGTASIAAKDQQAGV 471

Query: 480 TTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDF 539
      TTLKGAMAVMDIAETAITNLDQIRAD+G++QNQ+T T+NNI+VTQVN+K+AES IRDVDF
Sbjct: 472 TTLKGAMAVMDIAETAITNLDQIRADLGAVQNQITRTLNNISVTQVNIKSAESNIRDVDF 531

Query: 540 ASESANYSKANILAQSGSYAMAQANSSQQNVRLRLQ 575
      A+ESAN++K NILAQSGSYAM+QAN+ QQNV+RLRLQ
Sbjct: 532 AAESANFAKFNILAQSGSYAMSQANAVQQNVRLRLQ 567

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tr   Q6L5K9      Flagellin (Fragment) [flaA] [Campylobacter lari] 567 AA
                                align

```

Score = 754 bits (1947), Expect = 0.0

Identities = 406/576 (70%), Positives = 462/576 (79%), Gaps = 10/576 (1%)

```

Query: 1   GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
      GFRINTNVA+LNA+ N++LN+++LD+SLSRLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 1   GFRINTNVAASLNAQNNANLNSRALDSSLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60

Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDITIKTKATQAAQDGQSLKTRTMLQADINKLME 120
      GQAI+NGNDALGILQTADKAMDEQLKILDITIK KATQAAQDGQS KTR MLQADIN+LME
Sbjct: 61  GQAINNGNDALGILQTADKAMDEQLKILDITIKVKATQAAQDGQSTKTRNMLQADINRLME 120

Query: 121 ELDNIANTTTFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
      ELDNIANTT+FNKGQLLSG FTNQ FQIGA SNQT++A IGATQSSKIGVTRFETG+ S
Sbjct: 121 ELDNIANTTAFNGKQLLSGGFTNQSFQIGAQSNQTIQAGIGATQSSKIGVTRFETGSM SH 180

Query: 181 TSGVVGLTIKKNYNGIEDFKFDNVVISTSVGTGLGALAEIEINKSADKTGVRATYDVKTGTV 240
      +SGV LTIKKNYNGI+DFKF VVIS+SVGTG+GALAEIEIN+ AD TGVRA + V+TTG
Sbjct: 181 SSGVAQLTIKKNYNGIDDFKFQPVVISSSVGTGMGALAEIEINRVADVTGVRANFLVQTTGA 240

Query: 241 YAIKEGTTSQDFAINGVTIGKIEYKGDGNGSLISAINAVKDTTG VQASKDENGKLV LTS 300
      +IK   TSQDF INGV IG++EYKGDG NG+LISAIN+VKD TTGV+ASKD NG+LVL S
Sbjct: 241 GSIKADKTSQDFTINGVKIGEVEYKGDENGALISAINSVKDTTGVEASKDANGRLVLNS 300

Query: 301 ADGRGIKITGDIGVGSgilANQKENYGRSLVKNdGRDINISGTNLSAIGMGTTDMISQS 360
      DGRGI+ITG++GVGSG+L + +N+GRSLVKNdG+DI ISG+ LS IGMG DMISQ+
Sbjct: 301 RDGRGIEITGNMGVGSgVLKDDYKNFGRSLVKNdGKDILISGSGLSFIGMGAGDMISQA 360

Query: 361 SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXX 420
      SVSLRESKG I ADAMGFN+YKGGGK V T SSI AFM

```

```
Sbjct: 361 SVSLRESKGNIDTHVADAMGFNAYKGGGKMVIT--FSSIEAFMSSNGSGMSAGSGFSIGS 418
Query: 421 XKNLXXXXXXXXXXXXXXXXXXNTYVXXXXXXXXXXXXXQFAALKTTAA-NTTDETAGV 479
      K +                      T                      QFAA  TA+      D+ AGV
Sbjct: 419 GKEMSKIYNSGNLALV-----TVFSNAFGFSAKNDGSSQFAAFAGTASIAAKDQQAGV 471
Query: 480 TTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDF 539
      TTLKGAMAVMDIAETAITNLDQIRAD+G++QNQ+T T+NNI+VTQVN+K+AES IRDVDF
Sbjct: 472 TTLKGAMAVMDIAETAITNLDQIRADLGAVQNQITRTLNNISVTQVNIKSAESNIRDVDF 531
Query: 540 ASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
      A+ESAN++K NILAQSGSYAM+QAN+ QQNV+RLLQ
Sbjct: 532 AAESANFAKFNILAQSGSYAMSQANAVQQNVMRLLQ 567
```

```
tr    Q6L5L0      Flagellin (Fragment) [flaA] [Campylobacter lari] 566 AA
                                align
```

Score = 754 bits (1946), Expect = 0.0

Identities = 402/576 (69%), Positives = 466/576 (80%), Gaps = 11/576 (1%)

```
Query: 1   GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
      GFRINTNVA+LNA+ N++LN+++LD+SLSRLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 1   GFRINTNVAASLNAQNNANLNSRALDSSLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
      GQAI+NGNDALGILQTADKAMDEQLKILDTIK KATQAAQDGQS KTR MLQADIN+LME
Sbjct: 61  GQAINNGNDALGILQTADKAMDEQLKILDTIKVKATQAAQDGQSTKTRNMLQADINRLME 120
Query: 121 ELDNIANTTTFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
      ELDNIANTT+FNKGQLLSG FTNQ FQIGA SNQT++A+IGATQSSKIGVTRFETG+ S
Sbjct: 121 ELDNIANTTAFNGKQLLSGGFTNQSFQIGAQSNQTIQASIGATQSSKIGVTRFETGSM 180
Query: 181 TSGVVGLTIKNGYNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVRATYDVKTGTG 240
      +SGV LTIKNGYNGI+DFKF VVIS+SVGTG+GALAEIN+ +D TGVRA++ V+TTG
Sbjct: 181 SSGVAQLTIKNGYNGIDDFKFPVVISSSVGTGMGALAEINRVSDITGVRASFLVQTTGA 240
Query: 241 YAIKEGTTSQDFAINGVTIGKIEYKDGNGSLISAINAVKDTTGVQASKDENGKLVLT 300
      +IK TSQDF INGV IG++EYKDG NG+LISAIN+VKDTTGV+ASKD NG+LVL S
Sbjct: 241 GSIKADKTSQDFTINGVRIGEVEYKDGDENGALISAINSVKDTTGVASKDANGRLVLNS 300
Query: 301 ADGRGIKITGDIGVSGGILANQKENYGRSLSVKNDGRDINISGTNLSAIGMGTDMISQS 360
      DGRGI+ITG +G GSG+L + N+GRLSLVKNDG+DI ISG+NLSAIGMGT DMISQ+
Sbjct: 301 RDGRGIEITGSMGPGSGVLKDDYTNGRSLSVKNDGKDILISGSNLSAIGMGTDRDMISQA 360
Query: 361 SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXX 420
      S+SLRESKG I ADAMGFN+YKGGGK V T +++++M
Sbjct: 361 SISLRESKGNIDTHVADAMGFNAYKGGGKMVVT--FGTLASYMGSDGSGMSAGSGYSVNS 418
Query: 421 XKNLXXXXXXXXXXXXXXXXXXNTYVXXXXXXXXXXXXXQFAALKTTAA-NTTDETAGV 479
      KN+                      T                      QFAA  TA+      D+ AGV
Sbjct: 419 GKNMSALYEGNLAFV-----TAFSVAFGFSAKGDGTSQFAAFAGTASIAAKDQQAGV 470
Query: 480 TTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDF 539
      TTLKGAMAVMDIAETAITNLDQIRAD+G++QNQ+T+T+NNI+VTQVN+K+AES IRDVDF
Sbjct: 471 TTLKGAMAVMDIAETAITNLDQIRADLGAVQNQITATLNNISVTQVNIKSAESNIRDVDF 530
```

Query: 540 ASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
 A+ESAN++K NILAQSGSYAM+QAN+ QQNV+RLLQ
 Sbjct: 531 AAESANFAKFNILAQSGSYAMSQANAVQQNVMRLLQ 566

tr Q6L5K4 Flagellin (Fragment) [flaA] [Campylobacter lari] 567 AA
 align

Score = 751 bits (1940), Expect = 0.0
 Identities = 404/576 (70%), Positives = 462/576 (80%), Gaps = 10/576 (1%)

Query: 1 GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
 GFRINTNVA+LNA+ N++LN+++LD+SLSRLLSSGLRINSAADDASGMAIADSLRSQANTL
 Sbjct: 1 GFRINTNVASLNAQNNANLNSRALDSSLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60

Query: 61 GQAI SNGNDALGILQTADKAMDEQLKILDITIKTKATQAAQDGQSLKTRTMLQADINKLME 120
 GQAI+NGNDALGILQTADKAMDEQLKILDITIK KATQAAQDGQS KTR MLQADIN+LME
 Sbjct: 61 GQAINNGNDALGILQTADKAMDEQLKILDITIKVKATQAAQDGQSTKTRNMLQADINRLME 120

Query: 121 ELDNIAINTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
 ELDNIAINTT+FNGKQLLSG FTNQ FQIGA SNQT++A+IGATQSSKIGVTRFETG+ S
 Sbjct: 121 ELDNIAINTTAFNGKQLLSGGFTNQSFQIGAQSNQTIQASIGATQSSKIGVTRFETGSMH 180

Query: 181 TSGVVGLTIKKNYNGIEDFKFDNVVISTSVGTGLGALAE EINKSADKTGVRATYDVKTGGV 240
 +SGV LTIKKNYNGI+DFKF VVIS+SVGTG+GALAE EIN+ AD TGVRA + V+TTG
 Sbjct: 181 SSGVAQLTIKKNYNGIDDFKFQPVVIVSSSVGTGMGALAE EINRVADVTGVRANFLVQTTGA 240

Query: 241 YAIKEGTTSDFAINGVTIGKIEYKDG DNGSLISAINAVKDTTGVQASKDENGKLV LTS 300
 +IK TSQDF INGV IG++EYKDG DNG+LISAIN+VKDTTGV+ASKD NG+LVL S
 Sbjct: 241 GSIKADKTSQDFTINGVKIGEVEYKDG DENGALISAINSVKDTTGV EASKDANGRLV LNS 300

Query: 301 ADGRGIKITGDIGVSGILANQKENYGRSLVKN DGRDINISGTNLSAIGMGTTDMISQS 360
 DGRGI+ITG++ VGSG+L + +N+GRSLVKN DNG+DI ISG+ LS IGMG DMISQ+
 Sbjct: 301 RDGRGIEITGNMEVSGSVLKDDYKNFGRSLVKN DNGDKDILISGSLSFIMGAGDMISQA 360

Query: 361 SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXX 420
 S+SLRESKG I ADAMGFN+YKGGGK V T SSI AFM
 Sbjct: 361 SISLRESKGNIDTHIADAMGFNAYKGGGKMVVT--FSSIEAFMSSDGS GMSAGSGFSIGS 418

Query: 421 XKNLXXXXXXXXXXXXXXXXXNTYVXXXXXXXXXXXXXXXXXQFAALKTTAA-NTTDETAGV 479
 K + T QFAA TA+ D+ AGV
 Sbjct: 419 GKEMSKIYNSGNLALV-----TVFSNAFGFSAKNDGSSQFAAFAGTASIAAKDQQAGV 471

Query: 480 TTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDF 539
 TTLKGAMAVMDIAETAITNLDQIRAD+G++QNQ+T T+NNI+VTQVN+K+AES IRDVDF
 Sbjct: 472 TTLKGAMAVMDIAETAITNLDQIRADLGAVQNQITRTLNNISVTQVNIKSAESNIRDVDF 531

Query: 540 ASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
 A+ESAN++K NILAQSGSYAM+QAN+ QQNV+RLLQ
 Sbjct: 532 AAESANFAKFNILAQSGSYAMSQANAVQQNVMRLLQ 567

tr Q6L5K7 Flagellin (Fragment) [flaA] [Campylobacter lari] 563 AA
 align

tr Q6L5J6 **Flagellin (Fragment) [flaA] [Campylobacter lari]** 566 AA
align

Score = 749 bits (1935), Expect = 0.0
Identities = 400/576 (69%), Positives = 464/576 (80%), Gaps = 11/576 (1%)

Query: 1 GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
 GFRINTNVA+LNA+ N++LN+++LD+SLSRLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 1 GFRINTNVASLNAQNNANLNSRALDSSLRLSSGLRINSAADDASGMAIADSLRSQANTL 60

Query: 61 GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
 GQAI+NGNDALGILQTADKAMDEQLKILDTIK KATQAAQDGQS KTR MLQADIN+LME
Sbjct: 61 GQAINNGNDALGILQTADKAMDEQLKILDTIKVKATQAAQDGQSTKTRNMLQADINRLME 120

Query: 121 ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
 ELDNIANTT+FNGKQLLSG FTNQ FQIGA SNQT++A+IGATQSSKIGVTRFETG+ S
Sbjct: 121 ELDNIANTTAFNGKQLLSGGFTNQSFQIGAQSNTIQASIGATQSSKIGVTRFETGSMH 180

Query: 181 TSGVVGLTIKKNYNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVRATYDVKTGTG 240
 +SGV LTIKKNYNGI+DFKF VVIS+SVGTG+GALAEIN+ +D TGVRA++ V+TTG
Sbjct: 181 SSGVAQLTIKKNYNGIDDFKFQPVVISSSVGTGMGALAEINRVSDITGVRASFLVQTTGA 240

Query: 241 YAIKEGTTSDFAINGVTIGKIEYKDGNGSLISAINAVKDTTGVQASKDENGKLVLT 300
 +IK TSQDF INGV IG++EYKDG NG+LISAIN+VKDTTGV+ASKD NG+LVL S
Sbjct: 241 GSIKADKTSQDFTINGVRIGEVEYKDGDENGALISAINSVKDTTGVASKDANGRLVLNS 300

Query: 301 ADGRGIKITGDIGVSGGILANQKENYGRSLVKN DGRDINISGTNLSAIGMGTDMISQS 360
 DGRGI+ITG +G GSG+L + N+GRSLVKN DG+DI ISG+ LSAIGMGT DMISQ+
Sbjct: 301 RDGRGIEITGSMGPGSGVLKDDYT NFGRSLVKN DGKDILISGSLSAIGMGTADMISQA 360

Query: 361 SVSLRESKQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXXXX 420
 S+SLRESKG I ADAMGFN+YKGGGK V T +++++M
Sbjct: 361 SISLRESKGNIDTHVADAMGFNAYKGGGKMVVT--FGTLASYMGSDGSGMSAGSGYSVGS 418

Query: 421 XKNLXXXXXXXXXXXXXXXXXXXXNTYVXXXXXXXXXXXXXXXXXQFAALKTTAA-NTTDETAGV 479
 K + T QFAA TA+ D+ AGV
Sbjct: 419 GKEMSALYEGNLAFV-----TAFSVAFGFSAKGDGTSQFAAFAGTASIAAKDQQAGV 470

Query: 480 TTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDF 539
 TTLKGAMAVMDIAETAITNLDQIRAD+G++QNQ+T+T+NNI+VTQVN+K+AES IRDVDF
Sbjct: 471 TTLKGAMAVMDIAETAITNLDQIRADLGAVQNQITATLNNISVTQVNIKSAESNIRDVDF 530

Query: 540 ASESANYSKANILAQSGSYAMAQANSSQQNVRLRLQ 575
 A+ESAN++K NILAQSGSYAM+QAN+ QQNV+RLRLQ
Sbjct: 531 AAESANFAKFNILAQSGSYAMSQANAVQQNVMLRLQ 566

tr Q6L5L1 **Flagellin (Fragment) [flaA] [Campylobacter lari]** 566 AA
align

Score = 747 bits (1929), Expect = 0.0
Identities = 399/576 (69%), Positives = 463/576 (80%), Gaps = 11/576 (1%)

Query: 1 GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
 GFRINTNVA+LNA+ N++LN+++LD+SLSRLSSGLRINSAADDASGMAIADSLRSQANTL

```

Sbjct: 1   GFRINTNVASLNAQNNANLNSRALDSSSLRSLSSGLRINSAADDASGMAIADSLRSQANTL 60

Query: 61   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
           GQAI+NGNDALGILQTADKAMDEQLKILDTIK KATQAAQDGQS KTR MLQADIN+LME

Sbjct: 61   GQAINNGNDALGILQTADKAMDEQLKILDTIKVKATQAAQDGQSTKTRNMLQADINRLME 120

Query: 121  ELDNNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
           ELDNNIANTT+FNGKQLLSG FTNQ FQIGA SNQT++A+IGATQSSKIGVTRFETG+ S

Sbjct: 121  ELDNNIANTTAFNGKQLLSGGFTNQSFQIGAQSNQTIQASIGATQSSKIGVTRFETGSMH 180

Query: 181  TSGVVGLTIKKNYNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVRATYDVKTTGV 240
           +SGV LTIKKNYNGI+DFKF VVIS+SVGTG+GALAEIN+ +D TGVRA++ V+TTG

Sbjct: 181  SSGVAQLTIKKNYNGIDDFKFQPVVIVSSVGTGMGALAEINRVSDITGVRASFLVQTTGA 240

Query: 241  YAIKEGTTSQDFAINGVTIGKIEYKDGNGSLISAINAVKDTTGVQASKDENGKLVLS 300
           +IK TSQDF INGV IG++EYKDG NG+ ISAIN+VKDTTGV+ASKD NG+LVL S

Sbjct: 241  GSIKADKTSQDFTINGVRIGEVEYKDGDENGASISAINSVKDTTGVASKDANGRLVLNS 300

Query: 301  ADGRGIKITGDIGVSGILANQKENYGRSLVKNDRDINISGTNLSAIGMGTTDMISQS 360
           DGRGI+ITG +G GSG+L + N+GRSLVKNDRD+DI ISG+ LSAIGMGTTDMISQ+

Sbjct: 301  RDGRGIEITGSMGPGSGVLKDDYTNFGRSLVKNDRDILISGSLSAIGMGTTADMISQA 360

Query: 361  SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXX 420
           S+SLRESKG I ADAMGFN+YKGGGK V T +++++M

Sbjct: 361  SISLRESKGNIDTHVADAMGFNAYKGGGKMVVT--FGTLASYMGSDGSGMSAGSGYSVGS 418

Query: 421  XKNLXXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXXXQFAALKTTAA-NTTDETAGV 479
           K + T QFAA TA+ D+ AGV

Sbjct: 419  GKEMSALYEGNLAFV-----TAFSVAFGFSAKGDGTSQFAAFAGTASIAAKDQQAGV 470

Query: 480  TTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVSTINNITVTQVNVKAAESQIRDVDF 539
           TTLKGAMAVMDIAETAITNLDQIRAD+G++QNQ+T+T+NNI+VTQVN+K+AES IRDVDF

Sbjct: 471  TTLKGAMAVMDIAETAITNLDQIRADLGAVQNQITATLNNISVTQVNIKSAESNIRDVDF 530

Query: 540  ASESANYSKANILAQSGSYAMAQANSSQQNVRLRLQ 575
           A+ESAN++K NILAQSGSYAM+QAN+ QQNV+RLRLQ

Sbjct: 531  AAESANFAKFNILAQSGSYAMSQANAVQQNVRLRLQ 566

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tr   O85181          Flagellin B [flaB] [Campylobacter jejuni]          575 AA
                                           align

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Score = 747 bits (1928), Expect = 0.0

Identities = 405/578 (70%), Positives = 451/578 (77%), Gaps = 7/578 (1%)

```

Query: 1   GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
           GFRINTN+ ALNA ANS +NA+ LD SLSRLSSGLRINSAADDASGMAIADSLRSQA TL

Sbjct: 2   GFRINTNIGALNAHANSVVNARELDKSLRSLSSGLRINSAADDASGMAIADSLRSQAATL 61

Query: 61   GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
           GQAI+NGNDA+GILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LME

Sbjct: 62   GQAINNGNDAIGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLME 121

Query: 121  ELDNNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
           ELDNNIANTTSFNGKQLLSGNF NQEFQIGASSNQTVKATIGATQSSKIG+TRFETG +

Sbjct: 122  ELDNNIANTTSFNGKQLLSGNFINQEFQIGASSNQTVKATIGATQSSKIGLTRFETGGRIS 181

```



```

Query: 181 TSGVVGLTIKNGIEDFKFDNVVISTSVGTGLGALAEIINKSADKTGVRATYDVKTGTV 240
      +SG V T+KNYNGI+DF+F VVISTSVGTGLGALAEIINKSAD+TGVRAT+ V+T G+
Sbjct: 182 SSGEVQFTLKNYNGIDDFQFQKVVISSTSVGTGLGALAEIINKSADQTTGVRATFTVETGRM 241

Query: 241 YAIKEGTTSDFAINGVTIGKIEYKDGNGSLISAINAVKDTTGVQASKDENGKLVLTLS 300
      A++ GTTS FAINGV IG++ Y+DGD NG+L+SAIN+VKDTTGV+AS D NG+L+LTS
Sbjct: 242 AAVRAGTTSDTFAINGVKIGQVAYEDGDANGALVSAINSVKDTTGVASIDANGQLLLTS 301

Query: 301 ADGRGIKITGDIGVSGILANQKENYGRSLVKNDRDINISGTNLSAIGMGTTDMISQS 360
      +GRGIKI G IG G+ I + ENYGRSLVKNDRG+DI ISGT LS G G ++ ISQ
Sbjct: 302 REGRGIKIEGSIGGGAFINKDMMENYGRSLVKNDRGKDILISGTGLSFTGFGASNFISQV 361

Query: 361 SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXX 420
      SVSLRESKG+ A ADAMGF S G SSI+ +M
Sbjct: 362 SVSLRESKGRFDANTADAMGFGSVNKG----LVLAASSIADYMSAEGSGFSAGSGYSVGS 417

Query: 421 XKNLXXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXXXQFAALKTTAANT---TDETA 477
      K Y V QFA +KT+A N+ DETA
Sbjct: 418 GKGYSATLTANAIAISSASAISKIYNVSQSGFSSGSTLSQFATMKTSAGNSLGAKDETA 477

Query: 478 GVTTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDV 537
      GVTTLKGAMAVMDIAETA TNLDQIRADIGS+QNQ+ TINNITVTQVNVKAAES IRDV
Sbjct: 478 GVTTLKGAMAVMDIAETATTNLDQIRADIGSVQNQLQVTINNITVTQVNVKAAESTIRDV 537

Query: 538 DFASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
      DFA+ESAN+SK NILAQSGSYAM+QAN+ QQNVL+LLQ
Sbjct: 538 DFAAESANFSKYNILAQSGSYAMSQANAVQQNVLKLQ 575

```

tr Q6L5K0 **Flagellin (Fragment) [flaA] [Campylobacter lari]** 565 AA
align

Score = 746 bits (1926), Expect = 0.0

Identities = 400/576 (69%), Positives = 461/576 (79%), Gaps = 12/576 (2%)

```

Query: 1 GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
      GFRINTNVA+LNA+ N++LN+++LD+SLSRLSSGLRINSAADDASGMAIADSLRSQANTL
Sbjct: 1 GFRINTNVASLNAQNNANLNSRALDSSLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60

Query: 61 GQAISNGNDALGILQTADKAMDEQLKILDITIKTKATQAAQDGQSLKTRTMLQADINKLME 120
      GQAI+NGNDALGILQTADKAMDEQLKILDITIK KATQAAQDGQS KTR MLQADIN+LME
Sbjct: 61 GQAINNGNDALGILQTADKAMDEQLKILDITIKVKATQAAQDGQSTKTRNMLQADINRLME 120

Query: 121 ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
      ELDNIANTTSFNGKQLLSG FTNQ FQIGA SNQT++A+IGATQSSKIGVTRFETG+ +
Sbjct: 121 ELDNIANTTSFNGKQLLSGGFTNQSFQIGAQSNTIQASIGATQSSKIGVTRFETGSMK 180

Query: 181 TSGVVGLTIKNGIEDFKFDNVVISTSVGTGLGALAEIINKSADKTGVRATYDVKTGTV 240
      SGV LTIKNGYNGI+DFKF VVIS+SVGTG+GALAEIIN+ AD TGVRA + V+TTG
Sbjct: 181 ESGVAQLTIKNGYNGIDDFKFPVVISSSVGTGMGALAEIINRVADITGVRANFLVQTTGA 240

Query: 241 YAIKEGTTSDFAINGVTIGKIEYKDGNGSLISAINAVKDTTGVQASKDENGKLVLTLS 300
      +IK TSQDF INGV IG++EYK+GD NG+LISAIN+VKDTTGV+ASKD NG+LVL S
Sbjct: 241 GSIKADKTSQDFTINGVKIGEVEYKEGDENGALISAINSVKDTTGVASKDANGRLVLNS 300

```

Query: 301 ADGRGIKITGDIGVSGILANQKENYGRSLVKN DGRDINISGTNLSAIGMGTTDMISQS 360
DGRGI+ITG+IGVSGI+ + +N+GRSLVKN D+DI ISG+ LS IGMG DMISQ+
Sbjct: 301 RDGRGIEITGNIGVSGIMKDDYKNFGRSLVKN DGDILISGSLSFIMGGAADMISQA 360

Query: 361 SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXX 420
S+SLRESKG I ADAMGFN+YKGGGK + T ++I FM
Sbjct: 361 SISLRESKGNIDTHVADAMGFNAYKGGGKMIVTN--ANIGDFMSTNGMSAGTGYSVGSGK 418

Query: 421 XKNLXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXXXQFAA-LKTTAANTTDETAGV 479
+ + V QFAA L T + D+ AGV
Sbjct: 419 DMS-----KVYEGNLAFTVAFSVAFGFSVGN DGDATQFAAFLNTASIAAKDQQAGV 469

Query: 480 TTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDF 539
TTLKGAMAVMDIAETAITNLDQIRAD+G++QNQ+T T+NNI+VTQVN+K+AES IRDVDF
Sbjct: 470 TTLKGAMAVMDIAETAITNLDQIRADLGAVQNQITRTLNNISVTQVNIKSAESNIRDVDF 529

Query: 540 ASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
A+ESAN++K NILAQSGSYAM+QAN+ QQNV+RLLQ
Sbjct: 530 AAESANFAKFNILAQSGSYAMSQANAVQQNVMLLLQ 565

tr Q6L5K3 Flagellin (Fragment) [flaA] [Campylobacter lari] 567 AA
align

Score = 742 bits (1916), Expect = 0.0

Identities = 398/576 (69%), Positives = 458/576 (79%), Gaps = 10/576 (1%)

Query: 1 GFRINTNVAALNAKANS DLN A KSLDASL S R L S SGLRINSAADDASGMAIADSLRSQANTL 60
GFRINTNVA+LNA+ N++LN+++LD+SL S R L S SGLRINSAADDASGMATADSLRSQA TL
Sbjct: 1 GFRINTNVASLNAQNNANLNSRALDSS L S R L S SGLRINSAADDASGMAIADSLRSQAATL 60

Query: 61 GQAI SNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
GQAI+NGNDA+GILQTADKAMDEQLKILDTIK KATQAAQDGQS KTR MLQADIN+LME
Sbjct: 61 GQAINNGNDAIGILQTADKAMDEQLKILDTIKVKATQAAQDGQSTKTRNMLQADINRLME 120

Query: 121 ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
ELDNIANTT+FNGKQLLSGNFTNQEFQIGA SNQTVKA+IG TQSSKIGVTRFETG+ S
Sbjct: 121 ELDNIANTTAFNGKQLLSGNFTNQEFQIGA QSNQTVKASIGPTQSSKIGVTRFETGSM SH 180

Query: 181 TSGVVGLTIKKNYNGIEDFKFDNVVISTSVGTGLGALAE EINKSADKTGVRATYDVKT TGV 240
+SGV LTIKKNYNGI+DFKF VVIS+SVGTG+GALAE E IN+ AD TGVRA + V+TTGV
Sbjct: 181 SSGVAQLTIKKNYNGIDDFKFQPVVISSSVGTGMGALAE E INRVADVTGVRANFLVET TGV 240

Query: 241 YAIKEGTTSDFAINGVTIGKIEYKDG DNGSLISAINAVKDTTG VQASKDENGKLV LTS 300
AIK G TS DF INGV IG+IEY+D D NG+L++AIN+VKD+TGV+AS+D NG+LVL S
Sbjct: 241 GAIKAGVTSDDFTINGVKIGRIEYQSDSQNGALVAAINSVKDSTGVEASRDANGRLVLNS 300

Query: 301 ADGRGIKITGDIGVSGILANQKENYGRSLVKN DGRDINISGTNLSAIGMGTTDMISQS 360
DGRGI+ITGD+G G+G+L + +N+GRSLVKN D+DI ISG+ LS IGMG DMISQ+
Sbjct: 301 RDGRGIEITGDMGPGAGVLKDDYKNFGRSLVKN DGDILISGSLSFIMGAGADMISQA 360

Query: 361 SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXX 420
SVSLRESKG+I ADAMGFN+YKGGGK V T SSI AFM
Sbjct: 361 SVSLRESKGRIDPQADAMGFNAYKGGGKMVIT--FSSIEAFMSSNGSGMSAGSGFSIGS 418

Query: 421 XKNLXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXXXQFAALKTTAA-NTTDETAGV 479

```

      K +          T          QFAA  TA+    D+  GV
Sbjct: 419 GKEMSKIYNSGNLALV-----TVFSNAFGFSAKNDGSSQFAAFAGTASIAANDQAPGV 471

Query: 480 TTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDF 539
      TTLKGAMA+MDI ETA  NLD IRADIG++QNQ+T T+NNI+VTQVN+K+AES IRDVDF
Sbjct: 472 TTLKGAMAMMDIVETATANLDAIRADIGAVQNQITRTLNNISVTQVNIKSAESNIRDVDF 531

Query: 540 ASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
      A+ESAN++K NILAQSGSYAM+QAN+ QQNV+RLLQ
Sbjct: 532 AAESANFAKFNILAQSGSYAMSQANAVQQNVMRLLQ 567

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tr    P96751          Flagellin (Fragment) [flaA] [Campylobacter sp] 626 AA
                                align

```

Score = 605 bits (1560), Expect = e-172

Identities = 358/630 (56%), Positives = 418/630 (65%), Gaps = 60/630 (9%)

```

Query: 2   FRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLG 61
      FRINT+VAALNAKANSDLN+K+LD SL+RLSSGLRINSAADDASGMAIADSLR+QA+TLG
Sbjct: 1   FRINTHVAALNAKANSDLNSKALDQSLARLSSGLRINSAADDASGMAIADSLRTQASTLG 60

Query: 62  QAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLMEE 121
      QAI+NGNDA  ILQTADKAMDEQLKILDTIK KATQAAQDGQS KTR MLQADIN+LMEE
Sbjct: 61  QAINNGNDAASILQTADKAMDEQLKILDTIKVKATQAAQDGQSAKTRNMLQADINRLMEE 120

Query: 122 LDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSFT 181
      LDNIANTTSFNGKQLLSG F NQEFQIGA SNQT+KA+IGATQSSKIGVTRFETGA  +
Sbjct: 121 LDNIANTTSFNGKQLLSGGFINQEFQIGAQSNQTIKASIGATQSSKIGVTRFETGANVTS 180

Query: 182 SGVVGLTIKNGYNGIEDFKFDNVVISTSVGTGLGALAEIINKSADKTGVRATYDVKTGTVY 241
      S +  +TIKNGYNGI+DFK  NVVISTSVGTGLGALAEIIN+ AD+TGVRA+++V+T G
Sbjct: 181 SSIASMTIKNGYNGIDDFKIQNVVISTSVGTGLGALAEIINRVADRTGVRASFNVQTVGGA 240

Query: 242 AIKEGTTSDQFAINGVTIGKIEYKDGNGSLISAINAVKDDTTGVQASKDENG----- 294
      + +G+TS DF INGV IGKI+Y+ GD NGSL+S+INAVKDDTTGV+A+ +ENG
Sbjct: 241 PVLKGSTSDDFTINGVKIGKIDYESGDANGSLVSSINAVKDDTTGVEAALNENGQLVLTSR 300

Query: 295 -----KLVLTSADGRGIKITGD-IGVGSIGILANQ----- 322
      +L L  DGR I I+G  G  +  L +Q
Sbjct: 301 EGRGIKIEGDMGSGAGIAVNMRENYGRSLVKNDGRDIAISGTGFGFDNEKLVSQNSVSL 360

Query: 323 KENYGRSLSLVKNDGRDINISGTNLSAIGMGTDMISQSSVSLRESKGQISATNADAMGFN 382
      ++ G++S  D  N S  +++I +G T M  +  L +  +  +  GF+
Sbjct: 361 RDTKGQISQEIADAMGFN-SSNKVASIRIGVTAMSVLAGTGLSKETSLLYTAGS---GFS 416

Query: 383 SYKGGGKFVFTQNVSSI-----SAFMXXXXXXXXXXXXXXXXXXXXKNLXXXXXXXXXXXXX 436
      ++ K  I  SAF  L
Sbjct: 417 AFTISAKSQLNMVGQVIDLGPKHSAFSGGYTALGFTAGSGFSAINSALSMLMYSKMYGTQ 476

Query: 437 XXXXXXNTYVVXXXXXXXXXXXXXXXXXQFA-----ALKTTAANTT----DETAGVTTLKGA 485
      + V  LK+  T  ++TAGVTTLKGA
Sbjct: 477 TGAAKFSVAVAMSTADIKFVSTISTGGLSGLYNDGLKSGETRRTENIGQEQTAGVTTLKGA 536

Query: 486 MAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFASESAN 545
      MAVMD+AETAITNLD IRAD+GSIQNQ+++TINNITVTQVNVK+AES IRDVDFASESAN

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Sbjct: 537 MAVMDVAETAITNLDITRADLGSIQNQISATINNITVTQVNVKSAESTIRDVDFASESAN 596

Query: 546 YSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
 YSKANILAQSGSYAMAQAN+SQQNVLRLLQ

Sbjct: 597 YSKANILAQSGSYAMAQANASQQNVLRLLQ 626

tr P96752 **Flagellin [flaB] [Campylobacter sp]** 630 AA
align

Score = 598 bits (1541), Expect = e-169
 Identities = 358/630 (56%), Positives = 411/630 (64%), Gaps = 56/630 (8%)

Query: 1 GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
 GFRINTN+ ALNA ANS +NA +LD SL+RLSSGLRINSAADDASGMAIADSLRSQA TL

Sbjct: 2 GFRINTNIGALNAHANSVVNANALDKSLNRLSSGLRINSAADDASGMAIADSLRSQAATL 61

Query: 61 GQAI+NGNDA+GILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
 GQAI+NGNDA+GILQTADKAMDEQLKILDTIK KATQAAQDGQS KTR MLQADIN+LME

Sbjct: 62 GQAINNGNDAIGILQTADKAMDEQLKILDTIKVKATQAAQDGQSTKTRNMLQADINRLME 121

Query: 121 ELDNIANTTTFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
 ELDNIANTTTFNGKQLLSG F NQEFQIGA SNQT+KA+IGATQSSKIGVTRFETGA

Sbjct: 122 ELDNIANTTTFNGKQLLSGGFINQEFQIGAQSNTIKASIGATQSSKIGVTRFETGANVV 181

Query: 181 TSGVVGLTIKKNYNGIEDFKFDNVVISTSVGTGLGALAEIINKSADKTGVRATYDVKTGTGV 240
 SG+ LTIKKNYNG+EDFKF ++VISTSVGTGLGALAEIIN+ ADKTGVRA+++V+TTG

Sbjct: 182 QSGIASLTIKKNYNGLEDFKFRDIVISTSVGTGLGALAEIINRVADKTGVRASFNVQTTGG 241

Query: 241 YAIKEGTTSDFAINGVTIGKIEYKDGNGSLISAINAVKDTTGVQASKDENGKLV--- 297
 I G T +DF+INGV IGKIEY+ GD NG+L+S+INAVKDTTGV+A+ DENG LV

Sbjct: 242 APIIAGVTGEDFSINGVIIGKIEYQAGDANGALVSSINAVKDTTGVAAALDENGHLVLT 301

Query: 298 -----LTSADGRGIKITGD-IGVGSGILANQ----- 322
 L DGR I I+G G + L +Q

Sbjct: 302 REGRGIKIEGDMGSGAGIAVNMRENYGRSLVKNDRDIAISGTGFGFDNEKLVSQNSVS 361

Query: 323 -KENYGRSLVKNDRDINISGTNLSAIGMGTDM-----ISQSSVSLRESKGQISAT 374
 ++ G++S D N S +++I +G T M +S+ + L + SA

Sbjct: 362 LRDTKGQISQEIADAMGFN-SSNKVASIRIGVTAMSVLAGTGLSKETSLLYTAGSGFSAF 420

Query: 375 NADAMGFNSYKG-----GGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXKNLXXXXX 429
 A + G G K + F K

Sbjct: 421 TISAKSQLNMVGQVIDLGPKHSAFSGGYTALGFTAGSGFSAINSALSMLMYSKMYGTQTG 480

Query: 430 XXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXXXQFAAL----KTTAANTTDETAGVTTLKGA 485
 N + Q L K ++TAGVTTLKGA

Sbjct: 481 AAKFSVAIAMSTTNIQINSVSGTNGISGLYQTLGLEFGEKRIENIQEQTAGVTTLKGA 540

Query: 486 MAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFASESAN 545
 MAVMDIAETA NLDQIRADIGS+QNQ+ TINNITVTQVNVKAAES IRDVDF+ESAN

Sbjct: 541 MAVMDIAETATINLDQIRADIGSVQNQLQVTINNITVTQVNVKAAESTIRDVDFAAESAN 600

Query: 546 YSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
 +SK NILAQSGSYAM+QAN+ QQNVL+LLQ

Sbjct: 601 FSKYNILAQSGSYAMSQANAVQQNVLKLLQ 630

```
tr      Q84IC5      Flagellin (Fragment) [flaA] [Campylobacter lari] 490 AA
                                           align
Score = 534 bits (1375), Expect = e-150
Identities = 313/575 (54%), Positives = 379/575 (65%), Gaps = 85/575 (14%)
```

```

Query: 1   GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
          GFRINTN A+LNA+ N+ LN+++LD+SL+RLSSGLRINSAADDASG+AIADSL++QAN+L
Sbjct: 1   GFRINTNGASLNAQVNAGLNSRLDSSSLARLSSGLRINSAADDASGLAIADSLKTQANSL 60

Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDITIKTKATQAAQDGQSLKTRTMLQADINKLME 120
          GQAI+N NDA +LQ ADKAMDEQLKILDITIK KATQAAQDGQ+ KTR M+Q +INKLME
Sbjct: 61  GQAINNANDANSMLQIADKAMDEQLKILDITIKVKATQAAQDGQTAKTRAMIQGEINKLME 120

Query: 121 ELDNIANTTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
          ELDNIANTT++NGKQLLSG+F+N +FQIG +NQTV ATIG+T S+K+G TRFETGA
Sbjct: 121 ELDNIANTTTTYNGKQLLSGSFSNAQFQIGDKANQTVNATIGSTNSAKVGQTRFETGAVIT 180

Query: 181 TSGVVGLTIKNGYNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVRATYDVKTGTV 240
          + G TIK+Y+GI D+K D+V IS SVGTGLGALA EINK++DKTGVRAT V+T
Sbjct: 181 AAVSNGFTIKSYDGINDYKIDSVAISYSVGTGLGALAEINKASDKTGVRATATVQTISS 240

Query: 241 YAIKEGTTSDFAINGVTIGKIEYKDGNGSLISAINAVKDTTGVQASKDENGKVLVLT 300
          ++ G+T Q FAINGV IKG+ Y+ GD NG+L+SAINA KDTTGV+AS +
Sbjct: 241 GS LAAGSTGQTFaingvVIGKVVEAGDKNGALVSAINAKDTTGV EASIVD----- 292

Query: 301 ADGRGIKITGDIGVGSgilanQKENYGRSLVKNDRDINISGTNLSAIGMGTTDMISQS 360
          G+L L DGR I +SG+ + A+G
Sbjct: 293 -----GKLV LNSADGRGIKLSGS-IGALG----- 315

Query: 361 SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXX 420
          L E+ G++S D G F+ VS+I
Sbjct: 316 DQMLEENYGRSLVKN-----GSNIFISGTTVSNIGLGT AQMAEATVNLESIKGQI 367

Query: 421 XKNLXXXXXXXXXXXXXXXXXNTYVXXXXXXXXXXXXXQFAALKTTAANTTDETAGVT 480
          ++ F A+ T ++AGVT
Sbjct: 368 TADIASAMG-----FNAMSTADTAGKKQSAGVT 395

Query: 481 TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 540
          TL+GAMAVMDIA+TAI NLD IRA+IG+ QNQ+TSTINNI+VTQVNVKAAESQIRDVDFA
Sbjct: 396 TLQGAMAVMDIADTAIANLDTIRANIGATQNQITSTINNISVTQVNVKAAESQIRDVDFA 455

Query: 541 SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
          SESANYSKANILAQSGSYAMAQAN++ QNVLRLLQ
Sbjct: 456 SESANYSKANILAQSGSYAMAQANAASQNVLRLLQ 490

```

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tr   Q84IC7      Flagellin (Fragment) [flaA] [Campylobacter lari] 491 AA
                                align

```

Score = 523 bits (1346), Expect = e-147

Identities = 316/575 (54%), Positives = 374/575 (64%), Gaps = 84/575 (14%)

```

Query: 1   GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
          GFRINTN A+LNA+ N+ LN+++LD+SL+RLSSGLRINSAADDASG+AIADSL++QANTL
Sbjct: 1   GFRINTNGASLNAQVNAGLNSRLDSSSLARLSSGLRINSAADDASGLAIADSLKTQANTL 60

Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDITIKTKATQAAQDGQSLKTRTMLQADINKLME 120
          GQAI+N NDA +LQ ADKAMDEQLKILDITIK KATQAAQDGQS KTR M+Q +INKLME
Sbjct: 61  GQAINNANDANSMLQIADKAMDEQLKILDITIKVKATQAAQDGQSAKTRAMIQGEINKLME 120

Query: 121 ELDNIANTTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180

```

```

ELDNIANTTS+NGKQLLSG+F+N +FQIG +NQTV ATIGAT S KIG TRFETGA+
Sbjct: 121 ELDNIANTTSYNGKQLLSGSFSNAQFQIGDKANQTVNATIGATNSGKIGQTRFETGARIT 180

Query: 181 TSGVVGLTIKNGYNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVRATYDVKTGGV 240
SG GLTIK+Y+G+ DF V ISTS GTGLGALA EINKS+D TGVRAT V+T
Sbjct: 181 ASGSSGLTIKSYDGVNDFVIQPVITISTAGTGLGALAEINKSSDITGVRATATVQTIISS 240

Query: 241 YAIKEGTTSDFAINGVTIGKIEYKDGNGSLISAINAVKDTTGVQASKDENGKLVLTSS 300
+IK GTT ++F+INGV IGK+ +D D +G+L+SA + A KD G
Sbjct: 241 GSIKAGTTGENFSINGVIIGKVSVDNDKDGLVSA-----INAKKDTTGV----- 286

Query: 301 ADGRGIKITGDIGVSGILANQKENYGRSLVKN DGRDINISGTNLSAIGMGTTDMISQS 360
+ N G+L L DGR I + G+ +GT S S
Sbjct: 287 -----EASMVN-----GQLVLNSADGRGIELGGS-----LGT----SLS 316

Query: 361 SVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXXXX 420
V + G++S D G + GG + + S +A
Sbjct: 317 GVVASVNYGRSLVKN--GSDIIVNGGSLIGLSAGSKAA-----EA 357

Query: 421 XKNLXXXXXXXXXXXXXXXXXXXXXNTYVXXXXXXXXXXXXXXXXXXXXXQFAALKTTAANTTDETAGVT 480
NL F A+ T A +TAGVT
Sbjct: 358 TVNLESIKGEISADVASAMG-----FNAMTTAALAGKKQTAGVT 396

Query: 481 TLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDFA 540
TL+GAMAVMDIA+TAI NLD IRA+IG+ QNQ+TSTINNI+VTQVNVKAAESQIRDVDFA
Sbjct: 397 TLQGAMAVMDIADTAIANLDTIRANIGATQNQITSTINNISVTQVNVKAAESQIRDVDFA 456

Query: 541 SESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
SESANYSKANILAQSGSYAMAQAN++ QNVLRLLQ
Sbjct: 457 SESANYSKANILAQSGSYAMAQANAASQNVLRLLQ 491

```

tr Q84IC8 **Flagellin (Fragment) [flaA] [Campylobacter lari]** 492 AA
align

Score = 481 bits (1239), Expect = e-134

Identities = 255/391 (65%), Positives = 314/391 (80%), Gaps = 4/391 (1%)

```

Query: 1 GFRINTNVAALNAKANSDLNAKSLDASLRLSSGLRINSAADDASGMAIADSLRSQANTL 60
GFRINTN A+LNA+ N+ LN+++LD+SL+RLSSGLRINSAADDASG+AIADSL++QAN+L
Sbjct: 1 GFRINTNGASLNAQVNAGLNSRALDSSLARLSSGLRINSAADDASGLAIADSLKTQANSL 60

Query: 61 GQAI SNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
GQAI+N NDA +LQ ADKAMDEQLKILDTIK KATQAAQDGQ+ KTR M+Q +INKLME
Sbjct: 61 GQAINNANDANSMLQIADKAMDEQLKILDTIKVKATQAAQDGQTAKTRAMIQGEINKLME 120

Query: 121 ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
ELDNIANTTS+NGKQLLSG+F NQ+FQIG +NQTV ATIGAT S+KIG TRFETG++
Sbjct: 121 ELDNIANTTSYNGKQLLSGSFANQQFQIGDKANQTVNATIGATNSAKIGQTRFETGSKIS 180

Query: 181 TSGVVGLTIKNGYNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVRATYDVKTGGV 240
+ +G TIK+Y+G+ D++ V +S S GTGLGALA EINKS+D TGVRAT V+T
Sbjct: 181 AATNIGFTIKSYDGVNDYQIQA VAVSYSAGTGLGALAEINKSSDITGVRATATVQTIISS 240

Query: 241 YAIKEGTTSDFAINGVTIGKIEYKDGNGSLISAINAVKDTTGVQASKDENGKLVLTSS 300
IK GTT +DF+INGV IGK+E KDGD +G+L+SAINA KDTTGV+AS NG+LVL S

```

Sbjct: 241 GTIKTGTGTEGDFSINGVIIIGKVEVKDGDGKDALVSAINAKKDTTGVEASM-VNGQLVLNS 299

Query: 301 ADGRGIKITGDIGVG-SGILANQKENYGRSLSVKNDGRDINISGTNLSAIGMGTTDMISQ 359
 ADGRGI + G +G SG++A+ N+GRSLSVKNDG DI ISGTN S +G+G++ ++

Sbjct: 300 ADGRGIVLGGSLGTSLSGVVAS--ANFGRSLSVKNDGSDIIISGTNASQLGIGSSATTAE 357

Query: 360 SSVSLRESKGQISATNADAMGFNSYKGGGKF 390
 ++V+L KG+ISA A AMGFN+ F

Sbjct: 358 ATVNLESIKGEISADIASAMGFNAMSTAATF 388

tr Q93GT4 **Flagellin (Fragment) [flaA] [Campylobacter lari]** 486 AA
align

Score = 476 bits (1225), Expect = e-133
 Identities = 258/384 (67%), Positives = 310/384 (80%), Gaps = 9/384 (2%)

Query: 1 GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
 GFRINTN A+LNA+ N+ +N+++LD+SL+RLSSGLRINSAADDASGMAIADSLR+QA +L

Sbjct: 1 GFRINTNGASLNAQVNAGMNSRALDSSLARLSSGLRINSAADDASGMAIADSLRNQAASL 60

Query: 61 GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
 GQAI+NGNDA+GILQTADKAMDEQLKILDTIK KATQAAQDGQS KTR M+Q +INKLME

Sbjct: 61 GQAINNGNDAIGILQTADKAMDEQLKILDTIKVKATQAAQDGQSAKTRAMIQGEINKLME 120

Query: 121 ELDNIANTTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
 ELDNIANTT++NGKQLLSG F+NQ+FQIG +NQT+ ATIGATQS+KIG TRFETG++

Sbjct: 121 ELDNIANTTTTYNGKQLLSGAFSNQQFQIGDKANQTINATIGATQSAKIGQTRFETGSRIT 180

Query: 181 TSGVVGLTIKNGYIEDFKFDNVVISTSVGTGLGALAEIEINKSADKTGVRATYDVKTTGV 240
 SG G TIKNY+G+ DFK +V++STS GTGLGALA EINKS+DKTGVRAT V+T

Sbjct: 181 GSGNAGFTIKNYDGVNDFKIQSVILSTSAGTGLGALAEIEINKSSDKTGVRATATVQTISS 240

Query: 241 YAIKEGTTSQDFAINGVTIGKIEYKDGNGSLISAINAVKDTTGVQASKDENGKLVLT 300
 I+ G T F INGV IKG+ + GD +GSL++AINA KDTTGV+AS NG+LVL S

Sbjct: 241 GTIQAGNTGDTFTINGVVIGKVAQAGDKDGSVLAAINAKKDTTGVEASV-VNGQLVLNS 299

Query: 301 ADGRGIKITGDIGVGSGILAN-QKENYGRSLSVKNDGRDINISGTNLSAIGMGTTDMISQ 359
 ADGRGI+++ G+G+ + N NYGRSLSVKNDG DI ISG S G GT +++

Sbjct: 300 ADGRGIELS---GLGTALSGNIASVNYGRSLSVKNDGSDIIISGG--SGAGFGTA--VAE 352

Query: 360 SSVSLRESKGQISATNADAMGFNS 383
 ++V+L KGQISA A AMGFN+

Sbjct: 353 ATVNLESVKQISADIACAMGFNA 376

tr Q8RTY4 **Flagellin (Fragment) [flaA] [Campylobacter lari]** 491 AA
align

Score = 475 bits (1222), Expect = e-132
 Identities = 250/383 (65%), Positives = 309/383 (80%), Gaps = 3/383 (0%)

Query: 1 GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
 GFRINTN A+LNA+ N+ +N+++LD+SL+RLSSGLRINSAADDASG+AIADSL++QANTL

Sbjct: 1 GFRINTNGASLNAQVNAGMNSRALDSSLARLSSGLRINSAADDASGLAIADSLKTQANTL 60


```

Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
          GQAI+N NDA +LQ ADKAMDEQLKILDTIK KATQAAQDGQ+ KTR M+Q +INKLME
Sbjct: 61  GQAINNANDANSMLQIADKAMDEQLKILDTIKVKATQAAQDGQTAKTRAMIQGEINKLME 120

Query: 121 ELDNINANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
          ELDNINANTT++NGKQLLSG+F+NQ+FQIG +NQTV ATIG+T SSKIG TRFETGA+
Sbjct: 121 ELDNINANTTTYNGKQLLSGSFSNQFQIGDKANQTVNATIGSTNSSKIGQTRFETGARVT 180

Query: 181 TSGVVGLTIKKNYNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVRATYDVKTGTV 240
          G + +T+KNY+GI D+KF NV IST VGTGLGALA EINK++DKTGVR+ V+T
Sbjct: 181 GGGDISITLKNYDGIN DYKFQNVITISTGVTGLGALAEINKASDKTGVRASATVQTIST 240

Query: 241 YAIKEGTTSQDFAINGVTIGKIEYKDGNGSLISAINAVKDTTGVQASKDENGKLVLT 300
          A+ G+T + F INGV IKG+ +K+GD +G+L+SAINA KDTTGV+AS +GKLV L S
Sbjct: 241 AALTAGSTGEGFTINGVVIGKVVFKEGDKDGALVSAINAKKDTTGVEAS-IVDGKLV LNS 299

Query: 301 ADGRGIKITGDIGVSGILANQKENYGRSLVKN DGRDINISGTNLSAIGMGTTDMISQS 360
          ADGRGIK++G +G +A +ENYGR L+LVKN DGI +S T T +S++
Sbjct: 300 ADGRGIKLSGTLGALDTQIA--EENYGR LTLVKN DGS DIVSTTGAGFSTGATNAGLSEA 357

Query: 361 SVSLRESKGQISATNADAMGFNS 383
          +V+L KG+ISA A AMGFN+
Sbjct: 358 TVNLESIKGEISADIASAMGFNA 380

```

```

tr      Q56746      Flagellin [flag] [Wolinella succinogenes]      518 AA
                                align

```

Score = 474 bits (1221), Expect = e-132

Identities = 288/588 (48%), Positives = 363/588 (60%), Gaps = 86/588 (14%)

```

Query: 2  FRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLG 61
          F+INTNV+ALNA+A N+ L +SL +LSSGLRIN AADDASGMAIADSLR+QAN+LG
Sbjct: 3  FQINTNVSALNAQAQGGFNSTKLSSSLEKLSSGLRINKAADDASGMAIADSLRTQANS LG 62

Query: 62 QAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLMEE 121
          QAI N ND +GI+Q ADKAMDEQ+KILDTIKTKATQ+AQDGQ+ TR LQADIN+L+E
Sbjct: 63 QAIKNTNDGIGIVQIADKAMDEQIKILDTIKTKATQSAQDGQTTTTRKALQADINRLIEG 122

Query: 122 LDNINANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSFT 181
          LDNIA TTS+NG+ LLSG+FTN+EFQ+GA SNQT+KA+IGAT S KIG R ET Q
Sbjct: 123 LDNIAATTSYNGQSLLSGSFTNKEFQVGAYSNQTIKASIGATSSDKIGQVRLETSGQIVA 182

Query: 182 SG-----VVGLTIKKNYNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVRATYDV 235
          S V L N +G + ++V ISTS GTG+G L E INK++D V+A++ V
Sbjct: 183 SAGSSSLTSVALKFVNVDGTVNSVQLESVKIST SAGTGIGVLVETINKNSDALNVKASWSV 242

Query: 236 KTTGVYAIKEGTTSQDFAINGVTIGKI-EYKDGNGSLISAINAVKDTTGVQASKDENG 294
          + TG + GT + ING+TIG + + + D +G LI+AINAVKD TGV+AS DE G
Sbjct: 243 QATGSTNVASGTI-KGLEINGITIGTVTDVQKNDSDGRLIAAINAVKDQTGVEASIDEQG 301

Query: 295 KLVLT SADGRGIKI---TGDIGVSGILANQKENYGRSLVKN DGRDINISGTNLSAIGM 351
          +L L S DGR +++ + +G G + GT + G
Sbjct: 302 RLNLNSTDGRAVQVKTTASTILGGGSM-----GTASAGAGA 338

```

```

Query: 352 GTTDMISQSSVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXX 411
      T  I+ + + R+  QIS TNA+ +G + GG          S I A
Sbjct: 339 TTVGRITLRLDARDI--QISGTNANLVGLVASGGGAG-----SGIGAM----- 380

Query: 412 XXXXXXXXXXXXKXXXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXXXQFAALKTTAAN 471
      T V          A  A+
Sbjct: 381 -----AETTVNLRDVKGKFNENVASAAGANANASI 410

Query: 472 TTDET---AGVTTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNV 527
      TD      AGVT+LKGAM VMDIAE+AI  LD++R+D+GS+QNQ+TST+NNIT+TQVNV
Sbjct: 411 ATDNANGIGAGVTSLKGAMVMDIAESAIKMLDKVRSDLGSGVQNQMTSTVNNITITQVNV 470

Query: 528 KAAESQIRDVDFASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
      +AAES IR+VDFA+ES+NYSK NILAQ+GSYAM+QANSSQQN+LRLLQ
Sbjct: 471 QAAESNIREVDFAAESSNYSKLNILAQAGSYAMSQANSSQQNILRLLQ 518

```

tr Q93R24 **Flagellin (Fragment) [flaA] [Campylobacter lari]** 486 AA
align

Score = 474 bits (1220), Expect = e-132

Identities = 257/384 (66%), Positives = 309/384 (79%), Gaps = 9/384 (2%)

```

Query: 1  GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
      GFRINTN A+LNA+ N+ +N+++LD+SL+RLSSGLRINSAADDASGMAIADSLR+QA +L
Sbjct: 1  GFRINTNGASLNAQVNAGMNSRALDSSLARLSSGLRINSAADDASGMAIADSLRNQAASL 60

Query: 61  GQAI SNGN DALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
      GQAI+NGNDA+GILQTADKAMDEQLKILDTIK KATQAAQDGQS KTR M+Q +INKLME
Sbjct: 61  GQAINNGNDAIGILQTADKAMDEQLKILDTIKVKATQAAQDGQSAKTRAMIQGEINKLME 120

Query: 121 ELDN IANTT SFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
      ELDN IANTT++NGKQLLSG F+NQ+FQ+G +NQT+ ATIGATQS+KIG TRFETG++
Sbjct: 121 ELDN IANTTTTYNGKQLLSGAFSNQQFQVGDKANQTINATIGATQSAKIGQTRFETGSRIT 180

Query: 181 TSGVVGLTIK NYNGIEDFKFDNVVISTSVGTGLGALAE EINKSADKTGVRATYDVKTGTGV 240
      SG G TIKNY+G+ DFK +V++STS GTGLGALA EINKS+DKTGVRAT V+T
Sbjct: 181 GSGNAGFTIKNYDGVNDFKIQSVILSTSAGTGLGALAE EINKSSDKTGVRATATVQTISS 240

Query: 241 YAIKEGTTSDFAINGVTIGKIEYKDG DNGSLISAINAVKDTTGVQASKDENGKLV LTS 300
      I+ G T F INGV IGK+ + GD +GSL++AINA KDTTGV+AS NG+LVL S
Sbjct: 241 GTIQAGNTGDTFTINGVVIGKVA VQAGDKDGS LVAAINAKDTTGV EASV-VNGQLV LTS 299

Query: 301 ADGRGIKITGDIGVSGILAN-QKENYGRSLSVKNDGRDINISGTNLSAIGMGT TDMISQ 359
      ADGRGI+++ G+G+ + N NYGRSLSVKNDG DI ISG S G GT ++
Sbjct: 300 ADGRGIELS---GLGTALSGN IASVNYGRSLSVKNDGSDIIISGG--SGAGFGTA--AAE 352

Query: 360 SSVSLRESKGQISATNADAMGFNS 383
      ++V+L KGQISA A AMGFN+
Sbjct: 353 ATVNLESVKQISADIACAMGFNA 376

```

tr Q7M7N1 **FLAGELLIN B [FLAB] [Wolinella succinogenes]** 513 AA
align

Score = 473 bits (1217), Expect = e-132

Identities = 292/586 (49%), Positives = 365/586 (61%), Gaps = 85/586 (14%)

```

Query: 1  GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
          G+RINTNVAALNA A      N +SL++SL +LSSGLR+N AADDASGMAIADSLRSQA +L
Sbjct: 2  GYRINTNVAALNAHAIGVQNNRSLNSSLEKLSSGLRVNKAADDASGMAIADSLRSQAASL 61

Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
          GQA N NDA+GI+QTADKAMDEQ+KILDTIKTKA QAAQDGQ+ +TR LQ+DI +L+E
Sbjct: 62  GQATRNANDAIGIIQTADKAMDEQIKILDTIKTKAVQAAQDGQTTETRKALQSDILRLLE 121

Query: 121  ELDNIANTTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
          ELDNIANTTTSFNG+++LSG+F N+EFQIGA SN T+KA+IGAT S+KIG R ET + S
Sbjct: 122  ELDNIANTTTSFNGQEMLSGSFVNKEFQIGAYSNTTIKASIGATSSNKIGHVRLETSSISA 181

Query: 181  TSGV-----VGLTIKNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVR 230
          +S +          V + +G F+ + V ISTS GTG+GALAE INK+++ GVR
Sbjct: 182  SSMLASAGGSNLTEVAFKVLQVDGKNSFQLETVKISTSAGTGIGALAEVINKNSNVLGVR 241

Query: 231  ATYDVKTTGVYAIKEGTTSDFAINGVTIGKI-EYKDGNGSLISAINAVKD'TTGVQAS 289
          A+Y+V TG I+ GT + INGVITIG I + + D +G LI+AINAVK+ TGV+A
Sbjct: 242  ASYEVMTGSLPIQSGTVNT-LVINGVTIGTINDIQKNDADGKLINAINAVKEATGVEAY 300

Query: 290  KDENGKLVLTADGRGIKITGDIGVSGILANQKENYGRSLVKNDGRDINISGTNLSAI 349
          D +G+L L S DGR I ++ G G V G I SG++ + +
Sbjct: 301  TDISGRLTLKSTDGRAISVSTVSGAG-----VLGGGSFIGTSGSSHAIV 344

Query: 350  GMGTTDMISQSSVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXX 409
          G T ++ V IS TN +GF+S + G +T N+ + M
Sbjct: 345  GRLTLTRLNARDVL-----ISGTNFSHVGFHSAQ--GIAEYTVNLRDLRGEMNANIAS 395

Query: 410  XXXXXXXXXXXXXKNLXXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXXXQFAALKTTA 469
                                     A L +
Sbjct: 396  AAGAN-----ANLAIAS 407

Query: 470  ANTTDETAGVTTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKA 529
          AN AGVT+L GAM VMD+AE+A LD+IRAD+GS+Q Q+TSTINNITVTQVNV A
Sbjct: 408  ANANGIGAGVTSLAGAMIVMDMAESARIQLDKIRADLGSVQAQLTSTINNITVTQVNVAA 467

Query: 530  AESQIRDVDFASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
          AES+IRDVDFA ESA +SK NILAQSGS+AMAQAN+ QQNVL+LLQ
Sbjct: 468  AESEIRDVDFAEESATFSKHNILAQSGSFAMAQANTVQQNVLKLLQ 513

```

tr Q84IC9 Flagellin (Fragment) [flaA] [Campylobacter lari] 500 AA
align

Score = 471 bits (1213), Expect = e-131

Identities = 257/390 (65%), Positives = 307/390 (77%), Gaps = 8/390 (2%)

```

Query: 1  GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
          GFRINTN A+LNA+ N+ +N+++LD+SL+RLSSGLRINSAADDASG+AIAD+L++QANTL
Sbjct: 1  GFRINTNGASLNAQVNAGMNSRALDSSSLARLSSGLRINSAADDASGLAIADNLKTQANTL 60

Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
          GQAI+N NDA +LQ ADKAMDEQLKILDTIK KATQAAQDGQS KTR M+Q +I KLME

```

```

Sbjct: 61  GQAINNANDANSMLQIADKAMDEQLKILDTIKVKATQAAQDGQSAKTRAMIQGEITKLME 120

Query: 121  ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQ-S 179
           ELDNIANTTT++NGKQLLSG+F NQ+FQIG  +NQT+ ATIGAT S+KIG +RFETG  +
Sbjct: 121  ELDNIANTTTTYNGKQLLSGSFANQKFQIGDKANQTINATIGATYSAKIGQSRFETGQTIT 180

Query: 180  FTSGVVGLTIKNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVRATYDVKTTG 239
           ++G  +TIKNY+GI D+KF  V ISTS GTGLGALA EINK++D TGVRAT  V+T
Sbjct: 181  ASTGTASITIKNYDGINDYKFQAVTISTSGTGLGALAEINKASDITGVRATAIVQTVS 240

Query: 240  VYAI-KEGTTSQDFAINGVTIGKIEYKDGNGSLISAINAVKDDTTGVQASKDENGKLV 298
           AI  GTT  DFAINGV IKG+ YK  D  G+L+SAINA KDDTTGV+AS  +GKLV
Sbjct: 241  SGAIGASGTTGDDFAINGVVIGKVNYKANDKEGALVSAINAKDDTTGVEAS-IVDGKLV 299

Query: 299  TSADGRGIKITGDIGVG----SGILAN-QKENYGRSLSVKNDGRDINISGTNLSAIGMGT 353
           S DGRGI ITG +G G  AN  +ENYGRSLSVKNDG DI ISGT  S +G+G+
Sbjct: 300  NSIDGRGINITGSVGSGLSGDGAANLLRENYGRSLSVKNDGSDIISGTTASLLGVGS 359

Query: 354  TDMISQSSVSLRESKGQISATNADAMGFNS 383
           ++++V+L  KGQISA  A AMGFN+
Sbjct: 360  GGTAEATVNLESVKGQISADMASAMGFNA 389

```

```

tr  Q93GT1      Flagellin (Fragment) [flaA] [Campylobacter lari] 491 AA
                                align

```

Score = 469 bits (1207), Expect = e-131

Identities = 247/383 (64%), Positives = 308/383 (79%), Gaps = 3/383 (0%)

```

Query: 1  GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
           GFRINTN A+LNA+ N+ +N+++LD+SL+RLSSGLRINSAADDASG+AIADSL++QANTL
Sbjct: 1  GFRINTNGASLNAQVNAGMNSRALDSSSLARLSSGLRINSAADDASGLAIADSLKTQANTL 60

Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
           GQAI+N NDA  +LQ ADKAMDEQLKILDTIK KATQAAQDGQ+ KTR M+Q +INKLME
Sbjct: 61  GQAINNANDANSMLQIADKAMDEQLKILDTIKVKATQAAQDGQTAKTRAMIQGEINKLME 120

Query: 121  ELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
           ELDNIANTTT++NGKQLLSG+F+NQ+FQIG  +NQTV ATIG+T S+KIG TRFETGA+
Sbjct: 121  ELDNIANTTTTYNGKQLLSGSFSNQFQIGDKANQTVNATIGSTNSAKIGQTRFETGARVT 180

Query: 181  TSGVVGLTIKNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVRATYDVKTTGV 240
           + G + +T+KNY+GI D+KF +V +ST VGTGLGALA EINK +D+TGVR+  V+T
Sbjct: 181  SGGDIAITLKNYDGINDYKFQSVTVSTGVGTGLGALAEINKVSDQTGVRASATVQTIST 240

Query: 241  YAIKEGTTSQDFAINGVTIGKIEYKDGNGSLISAINAVKDDTTGVQASKDENGKLVLT 300
           A+  G+T + F INGV IKG+ +K GD +G+L+SAINA KDDTTGV+AS  +GKLV
Sbjct: 241  AALTAGSTGEGFTINGVVIGKVVFAGDKDGALVSAINAKKDDTTGVEAS-IVDGKLV 299

Query: 301  ADGRGIKITGDIGVGSGILANQKENYGRSLSVKNDGRDINISGTNLSAIGMGTDMISQS 360
           ADGRGIK++G IG  +A  +ENYGRSLSVKNDG DI +S T  T  +S++
Sbjct: 300  ADGRGIKLSGSIGDLDAQIA--EENYGRSLTVKNDGSDIVVSTTGAGFSTGATNAGLSEA 357

Query: 361  SVSLRESKGQISATNADAMGFNS 383
           +V+L  KG+ISA  A AMGFN+
Sbjct: 358  TVNLESIKGEISADIASAMGFNA 380

```

tr Q84IC3 **Flagellin (Fragment) [flaA] [Campylobacter lari]** 487 AA
align

Score = 469 bits (1206), Expect = e-131

Identities = 253/384 (65%), Positives = 310/384 (79%), Gaps = 9/384 (2%)

Query: 1 GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
GFRINTN A+LNA+ N+ +N+++LD+SL+RLSSGLRINSAADDASG+AIADSL++QAN+L
Sbjct: 1 GFRINTNGASLNAQVNAGMNSRALDSSLARLSSGLRINSAADDASGLAIADSLKTQANS 60

Query: 61 GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
GQAI+N NDA +LQ ADKAMDEQLKILDTIK KATQAAQDGQS KTR M+Q +INKLME
Sbjct: 61 GQAINNANDANSMLQIADKAMDEQLKILDTIKVKATQAAQDGQSAKTRAMIQGEINKLME 120

Query: 121 ELDNIANTTTFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
ELDNIANTT++NGKQLLSG F+NQ+FQIG +NQT+ ATIGATQS+KIG TRFETG++
Sbjct: 121 ELDNIANTTTYNKQLLSGAFSNQQFQIGDKANQTINATIGATQSAKIGQTRFETGSRIT 180

Query: 181 TSGVVGLTIKKNYNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVRATYDVKTTGV 240
SG G TIKNY+G+ DFK +V++STS GTGLGALA EINKS+DKTGVRAT V+T
Sbjct: 181 GSGNAGFTIKNYDGVNDFKIQSVILSTSAGTGLGALAEINKSSDKTGVRATATVQTISS 240

Query: 241 YAIKEGTTSDFAINGVTIGKIEYKDGNGSLISAINAVKDTTGVQASKDENGKLVLS 300
I+ G T F INGV IKG+ + GD +GSL++AINA KDTTGV+AS NG+LVL S
Sbjct: 241 GTIQAGNTGDTFTINGVVIGKVAVQAGDKDGS LVAAINAKKDTTGVVEASV-VNGQLVLNS 299

Query: 301 ADGRGIKITGDIGVGSGILAN-QKENYGRSLSLVKNDGRDINISGTNLSAIGMGTDMISQ 359
ADGRGI+++ G+G+ + N NYGRSLSLVKNDG DI ISG SA+G+GT ++
Sbjct: 300 ADGRGIELS---GLGTALSGNIASVNYGRSLSLVKNDGSDIIISG--SAVGLGTA--TAE 352

Query: 360 SSVSLRESKGQISATNADAMGFNS 383
++V+L KGQI+A+ A AMGFN+
Sbjct: 353 ATVNLESVKGQIAASIACAMGFNA 376

tr Q84IC6 **Flagellin (Fragment) [flaA] [Campylobacter lari]** 487 AA
align

Score = 468 bits (1205), Expect = e-130

Identities = 253/384 (65%), Positives = 310/384 (79%), Gaps = 9/384 (2%)

Query: 1 GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
GFRINTN A+LNA+ N+ +N+++LD+SL+RLSSGLRINSAADDASG+AIADSL++QAN+L
Sbjct: 1 GFRINTNGASLNAQVNAGMNSRALDSSLARLSSGLRINSAADDASGLAIADSLKTQANS 60

Query: 61 GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
GQAI+N NDA +LQ ADKAMDEQLKILDTIK KATQAAQDGQS KTR M+Q +INKLME
Sbjct: 61 GQAINNANDANSMLQIADKAMDEQLKILDTIKVKATQAAQDGQSAKTRAMIQGEINKLME 120

Query: 121 ELDNIANTTTFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
ELDNIANTT++NGKQLLSG F+NQ+FQIG +NQT+ ATIGATQS+KIG TRFETG++
Sbjct: 121 ELDNIANTTTYNKQLLSGAFSNQQFQIGDKANQTINATIGATQSAKIGQTRFETGSRIT 180

Query: 181 TSGVVGLTIKNGYNGIEDFKFDNVVISTSVGTGLGALAE EINKSADKTGVRATYDVKTTGV 240
 SG G TIKNY+G+ DFK +V++STS GTGLGALA EINKS+DKTGVRAT V+T
 Sbjct: 181 GSGNAGFTIKNYDGVNDFKIQSVILSTSAGTGLGALAE EINKSSDKTGVRATATVQTISS 240

Query: 241 YAIKEGTTSDFAINGVTIGKIEYKDGNGSLISAINAVKDTTGVQASKDENGKLVLTLS 300
 I+ G T F INGV IGK+ + GD +GSL++AINA KDTTGV+AS NG+LVL S
 Sbjct: 241 GTIQAGNTGDPFTINGVVIGKVAVQAGDKDGS LVAAINAKKDTTGVEASV-VNGQLVLNS 299

Query: 301 ADGRGIKITGDIGVSGILAN-QKENYGRSLSVKNDGRDINISGTNLSAIGMGTDDMISQ 359
 ADGRGI+++ G+G+ + N NYGRSLSVKNDG DI ISG SA+G+GT ++
 Sbjct: 300 ADGRGIELS---GLGTALSGNIASVNYGRSLSVKNDGDDIIISGG--SAVGLGTA--TAE 352

Query: 360 SSVSLRESKGQISATNADAMGFNS 383
 ++V+L KGQI+A+ A AMGFN+
 Sbjct: 353 ATVNLESVKGQIAASIACAMGFNA 376

tr Q84IC2 **Flagellin (Fragment) [flaA] [Campylobacter lari]** 500 AA
align

Score = 466 bits (1199), Expect = e-130
 Identities = 257/391 (65%), Positives = 310/391 (78%), Gaps = 10/391 (2%)

Query: 1 GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
 GFRINTN A+LNA+ N+ +N+++LD+SL+RLSSGLRINSAADDASG+AIADSL++QANTL
 Sbjct: 1 GFRINTNGASLNAQVNAGINSRALDSSLARLSSGLRINSAADDASGLAIADSLKTQANTL 60

Query: 61 GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
 GQAI+N NDA +LQ ADKAMDEQLKILDTIK KATQAAQDGQS KTR M+Q +INKLME
 Sbjct: 61 GQAINNANDANSMLQIADKAMDEQLKILDTIKVKATQAAQDGQSAKTRAMIQGEINKLME 120

Query: 121 ELDNIANTTSFN-GKQLLSG-NFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQ 178
 ELDNIANTT++N GKQLLSG F+NQ+FQIG +NQT+ ATIGAT S+KIG +RFETG Q
 Sbjct: 121 ELDNIANTTTTYNTGKQLLSGAYFSNQFQIGDKANQTINATIGATYSAKIGQSRFETG-Q 179

Query: 179 SFTSGVVGLTIKNGYNGIEDFKFDNVVISTSVGTGLGALAE EINKSADKTGVRATYDVKTT 238
 T+ +TIKNY+GI DFK +V +STS GTGLGALA EINKS+DKTGVRAT V+T
 Sbjct: 180 RITASRASITIKNYDGINDFKIQSVTLSTSAGTGLGALAE EINKSSDKTGVRATATVQTI 239

Query: 239 GVIYAI-KEGTTSDFAINGVTIGKIEYKDGNGSLISAINAVKDTTGVQASKDENGKLV 297
 AI G T DF INGV IGK+ YK D +G+L+SAINA KDTTGV+AS +GKLV
 Sbjct: 240 SSGAIGASNTGDDFTINGVVIGKVAYKANDKD GALVSAINAKKDTTGVEAS-IVDGKLV 298

Query: 298 LTSADGRGIKITGDIGVG----SGILAN-QKENYGRSLSVKNDGRDINISGTNLSAIGMG 352
 L SADGRGI+++G +G G S +AN ENYGRSLSVKNDG DI +SGT S +G+G
 Sbjct: 299 LNSADGRGIELSGSLGSLGSGDSAAIANLLSENYGRSLSVKNDGSDIIVSGTTASLLGVG 358

Query: 353 TDDMISQSSSVSLRESKGQISATNADAMGFNS 383
 + ++++V+L KGQI+A A AMGFN+
 Sbjct: 359 SGGATAEATVNLESVKGQIAADIASAMGFNA 389

tr Q93GT2 **Flagellin (Fragment) [flaA] [Campylobacter lari]** 487 AA
align

Score = 462 bits (1190), Expect = e-129
 Identities = 253/383 (66%), Positives = 306/383 (79%), Gaps = 7/383 (1%)

```

Query: 1   GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
          GFRINTN A+LNA+ N+ +N+++LD+SL+RLSSGLRINSAADDASG+AIADSL++QAN+L
Sbjct: 1   GFRINTNGASLNAQVNAGMNSRALDSSLARLSSGLRINSAADDASGLAIADSLKTQANSL 60

Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
          GQAI+N NDA +LQ ADKAMDEQLKILDTIK KATQAAQDGQ+ KTR M+Q +INKLME
Sbjct: 61  GQAINNANDANSMLQIADKAMDEQLKILDTIKVKATQAAQDGQTAKTRAMIQGEINKLME 120

Query: 121 ELDNIAINTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
          ELDNIA TT++NGKQLLSG F+NQ+FQIG +NQTV ATIG+T SSKIG TRFETG++
Sbjct: 121 ELDNIATTTTYNGKQLLSGAFSNQQFQIGDKANQTVNATIGSTNSSKIGQTRFETGSRVT 180

Query: 181 TSGVVGLTIKNGYIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVRATYDVKTGTG 240
          G +G TIKNY+G+ DFK VVISTS GTGLGALA EINKS+DKTGVRAT V+T
Sbjct: 181 AGGNLGFTIKNYDGVNDFKVQPVVISTSAGTGLGALAEINKSSDKTGVRATAVVQTISS 240

Query: 241 YAIKEGTTSDFAINGVTIGKIEYKDGNGSLISAINAVKDTTGVQASKDENGKLVLT 300
          I+ G T F INGV IGK+ + GD +GSL++AINA KDTTGV+AS NG+LVL S
Sbjct: 241 GTIQAGNTGDTFTINGVVIGKVAVRAGDKDGSVAAINAKKDTTGVVEASV-VNGQLVLNS 299

Query: 301 ADGRGIKITGDIGVGSGILANQKENYGRSLSVKNDGRDINISGTNLSAIGMGTTDMISQS 360
          ADGRGI+I+G SG +A+ NYGRSLSVKNDG DI ISG S +G+GT +++
Sbjct: 300 ADGRGIEISGLSALSGLHIAS--VNYGRSLSVKNDGSDIIISGG--STVGLGTA--TAEA 353

Query: 361 SVSLRESKGQISATNADAMGFNS 383
          +V+L KGQI+A+ A AMGFN+
Sbjct: 354 TVNLESVKGQIAASIACAMGFNA 376
  
```

tr Q84IC1 **Flagellin (Fragment) [flaA] [Campylobacter lari]** 487 AA
align

Score = 462 bits (1189), Expect = e-129
 Identities = 253/383 (66%), Positives = 306/383 (79%), Gaps = 7/383 (1%)

```

Query: 1   GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
          GFRINTN A+LNA+ N+ +N+++LD+SL+RLSSGLRINSAADDASG+AIADSL++QAN+L
Sbjct: 1   GFRINTNGASLNAQVNAGMNSRALDSSLARLSSGLRINSAADDASGLAIADSLKTQANSL 60

Query: 61  GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
          GQAI+N NDA +LQ ADKAMDEQLKILDTIK KATQAAQDGQ+ KTR M+Q +INKLME
Sbjct: 61  GQAINNANDANSMLQIADKAMDEQLKILDTIKVKATQAAQDGQTAKTRAMIQGEINKLME 120

Query: 121 ELDNIAINTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
          ELDNIAINTT++NGKQLLSG F+NQ+FQIG +NQTV ATIG+T SSKIG TRFETG++
Sbjct: 121 ELDNIAINTTTTYNGKQLLSGAFSNQQFQIGDKANQTVNATIGSTNSSKIGQTRFETGSRVT 180

Query: 181 TSGVVGLTIKNGYIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVRATYDVKTGTG 240
          G +G TIKNY+G+ DFK VVISTS GTGLGALA EINKS+DKTGVRAT V+T
Sbjct: 181 AGGNLGFTIKNYDGVNDFKVQPVVISTSAGTGLGALAEINKSSDKTGVRATAVVQTISS 240

Query: 241 YAIKEGTTSDFAINGVTIGKIEYKDGNGSLISAINAVKDTTGVQASKDENGKLVLT 300
          I+ G T INGV IGK+ + GD +GSL++AINA KDTTGV+AS NG+LVL S
  
```

Sbjct: 241 GTIQAGNTGDTLTINGVVIGKVAVQAGDKDGSLSVAAINAKKDTTGVEASV-VNGQLVLNS 299

Query: 301 ADGRGIKITGDIGVGSGILANQKENYGRSLVKNKGRDINISGTNLSAIGMGTTDMISQS 360
 ADGRGI+I+G SG +A+ NYGRSLVKNKDG DI ISG S +G+GT +++
 Sbjct: 300 ADGRGIEISGLGSALSGHIAS--VNYGRSLVKNKDGSDIIISGG--STVGLGTA--TAEA 353

Query: 361 SVSLRESKGQISATNADAMGFNS 383
 +V+L KGQI+A+ A AMGFN+
 Sbjct: 354 TVNLESVKQIAASIACAMGFNA 376

tr Q93GT3 **Flagellin (Fragment) [flaA] [Campylobacter lari]** 492 AA
align

Score = 456 bits (1173), Expect = e-127

Identities = 249/390 (63%), Positives = 305/390 (77%), Gaps = 6/390 (1%)

Query: 1 GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTL 60
 GFRINTN A+LNA+ N+ LN+++LD SL+RLSSGLRINSAADDASG+AIAD+L++QANTL
 Sbjct: 1 GFRINTNGASLNAQVNAGLNSRALDQSLNRLSSGLRINSAADDASGLAIADNLKTQANTL 60

Query: 61 GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
 GQAI+N NDA +LQ ADKAMDEQLKILDTIK KATQAAQDGQ+ KTR M+Q +INKLME
 Sbjct: 61 GQAINNANDANSMLQIADKAMDEQLKILDTIKVKATQAAQDGQTAKTRAMIQGEINKLME 120

Query: 121 ELDNIANTTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
 ELDNIANTT++NGKQLLSG+F+NQ+FQIG +NQTV ATIG+T S+KIG TRFETGA+
 Sbjct: 121 ELDNIANTTTTYNGKQLLSGSFSNQFQIGDKANQTVNATIGSTNSAKIGQTRFETGARVT 180

Query: 181 TSGVVGLTIKNGYNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVRATYDVKTGTV 240
 S V + Y+GI D++F +V +S SVGTGLGALA EINK AD+TGVRA+ V+T
 Sbjct: 181 GSTDVAFKLLRYDGINDYQFQSVAVSYSVGTGLGALAEINKVADQTGVRASATVQTISS 240

Query: 241 YAIKEGTTSDFAINGVTIGKIEYKDGNGSLISAINAVKDTTGVQASKDENGKLVLS 300
 A+ G+T + FAINGV IGK++Y+ GD +G+L+SAINA KDTTGV+AS +GKLVL S
 Sbjct: 241 GALTAGSTGEGFAINGVVIGKVYQAGDKDGALVSAINAKKDTTGVEAS-IVDGKLVLS 299

Query: 301 ADGRGIKITGDIGVGSGILANQ--KENYGRSLVKNKGRDINISGTNLSAIGMGTTDMIS 358
 ADGRGIK++G IG G L Q +ENYGRSLVKNKDG DI IS T T +S
 Sbjct: 300 ADGRGIKLSGTIG---GDLEAQMVEENYGRSLTLVKNKDGSDIIISTTAGGFSANATAAGLS 356

Query: 359 QSSVSLRESKGQISATNADAMGFNSYKGGG 388
 +++ +L KG+ISA A AMGFN+ G
 Sbjct: 357 EATTNLESIKGEISADIASAMGFNAMSTAG 386

tr Q46462 **Flagellin (Fragment) [fla2] [Campylobacter upsaliensis]** 436 AA
align

Score = 451 bits (1160), Expect = e-125

Identities = 234/306 (76%), Positives = 263/306 (85%), Gaps = 3/306 (0%)

Query: 78 DKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLMEELDNIANTTTSFNGKQLL 137
 DKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LMEELDNIANTTTSFNGKQLL
 Sbjct: 1 DKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLMEELDNIANTTTSFNGKQLL 60

Query: 138 SGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSFTSGVVGLTIKNYNGIED 197
SG F NQEFQIG+SSNQ+KATIGA+QSSKIG+TRFETG Q SG +TIKNYNGI+D
Sbjct: 61 SGGFINQEFQIGSSSNQTIKATIGASQSSKIGLTRFETGTQVIQSGTAQMTIKNYNGIDD 120

Query: 198 FKFDNVVISTSVGTGLGALAEIINKSADKTGVRATYDVKTGTVYAIKEGTTSDFAINGV 257
FKF V ISTDVGTGLGALAEIIN+ ADKTGVR++++V+T G +I +GTT+ FAINGV
Sbjct: 121 FKFAQVKISTSVGTGLGALAEIINRVADKTGVRASFNVQTVGARSIMKGTNDFAINGV 180

Query: 258 TIGKIEYKDGNGSLISAINAVKDTTGVQASKDENGKLVLTSDGRGIKITGDIGVGSG 317
TIGK+ Y++ D NG+LI+AINAVKDTTGVQA+ DE GKLVLTSADGRGIKITG IG G+G
Sbjct: 181 TIGKVAYENNDNGALIAAINAVKDTTGVQAALDEEGKLVLTSDGRGIKITGSIGPGAG 240

Query: 318 ILANQKENYGRSLSVKNDGRDINISGTNLSAIGMGTDMISQSSVSLRESKGQISATNAD 377
I N +ENYGRSLSVKNDGRDI I GT +G ++SQSS+SLRE+KGQIS A+
Sbjct: 241 IALNMQENYGRSLSVKNDGRDIAIEGT--GVGFDNDKLVSQSSISLRETKGQISKDLAE 297

Query: 378 AMGFNS 383
AMGFNS
Sbjct: 298 AMGFNS 303

tr Q46461 **Flagellin (Fragment) [fla1] [Campylobacter upsaliensis]** 436 AA
align

Score = 446 bits (1147), Expect = e-124

Identities = 230/306 (75%), Positives = 261/306 (85%), Gaps = 3/306 (0%)

Query: 78 DKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLMEELDNIAANTTSFNGKQLL 137
DKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LMEELDNIAANTTSFNGKQLL
Sbjct: 1 DKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLMEELDNIAANTTSFNGKQLL 60

Query: 138 SGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSFTSGVVGLTIKNYNGIED 197
SG F NQEFQIG+ SNQT+KATIG TQS+KIG+TRFETGAQ S V + IKNYNG+ED
Sbjct: 61 SGGFINQEFQIGSQSNQTIKATIGPTQSNKIGLTRFETGAQIIKSSEVEMVIKNYNGLED 120

Query: 198 FKFDNVVISTSVGTGLGALAEIINKSADKTGVRATYDVKTGTVYAIKEGTTSDFAINGV 257
FKF + ISTDVGTGLGALAEIIN+ ADKTGVR++++V+T G + +GTT+++FAINGV
Sbjct: 121 FKFPKIKISTSVGTGLGALAEIINRVADKTGVRASFNVQTVGARPVMKGTNNENFAINGV 180

Query: 258 TIGKIEYKDGNGSLISAINAVKDTTGVQASKDENGKLVLTSDGRGIKITGDIGVGSG 317
TIGK+ Y++ D NG+LI+AINAVKDTTGVQA+ DE GKLVLTSADGRGIKITG IG G+G
Sbjct: 181 TIGKVAYENNDNGALIAAINAVKDTTGVQAALDEEGKLVLTSDGRGIKITGSIGPGAG 240

Query: 318 ILANQKENYGRSLSVKNDGRDINISGTNLSAIGMGTDMISQSSVSLRESKGQISATNAD 377
I N +ENYGRSLSVKNDGRDI I GT G ++SQSS+SLRE+KGQIS A+
Sbjct: 241 IALNMQENYGRSLSVKNDGRDIAIEGT--GVGFDNDKLVSQSSISLRETKGQISKDLAE 297

Query: 378 AMGFNS 383
AMGFNS
Sbjct: 298 AMGFNS 303

sp Q9XB38 **Flagellin A [flaA] [Helicobacter felis]** 512 AA
FLAA_HELFE align

tr Q7X2D1 **Flagellin A [flaA] [Helicobacter pylori (Campylobacter pylori)]** 510
AA
align

Score = 443 bits (1140), Expect = e-123
Identities = 265/576 (46%), Positives = 346/576 (60%), Gaps = 72/576 (12%)

Query: 2 FRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLG 61
F++NTN+ A+NA S L +L SL RLSSGLRIN AADDASGM +ADSLRSQAN+LG
Sbjct: 3 FQVNTNINAMNAHVQSALTQNALKTSLERLSSGLRINKAADDASGMTVADSLRSQANSLG 62

Query: 62 QAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLMEE 121
QAI+N ND +GI+Q ADKAMDEQLKILDT+K KATQAAQDGQ+ ++R +Q+DI +L++
Sbjct: 63 QAIANTNDGMGIIQVADKAMDEQLKILDTVKVKATQAAQDGQTTESRKAIQSDIVRLIQG 122

Query: 122 LDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSFT 181
LDNI NTT++NG+ LLSG FTN+EFQ+GA SNQ++KA+IG+T S KIG R TGA
Sbjct: 123 LDNIGNTTTTYNGQALLSGQFTNKEFQVGAYSNQSIKASIGSTTSKIGQVRIATGALITA 182

Query: 182 SGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEIINKSADKTGVRATYDVKTGTGVY 241
SG + LT K +G+ D ++V IS+S GTG+G LAE INK++++TGV+A V TT
Sbjct: 183 SGDISLTFKQVDGVNDVTLESVKISSAGTGIGVLAEVINKNSNQTGVKAYASVITTS DV 242

Query: 242 AIKEGTTSQDFAINGVTIGKI-EYKDG DNGSLISAINAVKDTTGVQASKDENGKLV LTS 300
A++ G+ S + +NG+ +G I + K D +G L++AINAV TGV+A D+NG
Sbjct: 243 AVQSGSLS-NLTLNGIHLGNIA DIKKNDSDGRLVAAINAVTSETGVEAYTDQNG----- 295

Query: 301 ADGRGIKITGDIGVSGILANQKENYGRSLVKN DGRDINISGTNLSAIGMGT TDMIS-- 358
RL+L DGR I I ++S G M++
Sbjct: 296 -----RLNLRSLDGRGIEIKTDSVSN-GPSALTMVNGG 327

Query: 359 QSSVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXX 418
Q + G++S T DA NV S S
Sbjct: 328 QDLTKGSTNYGRSLSLTRLDAKSI-----NVVSASDSQHLGFTAIGFGESQVA 374

Query: 419 XXXKNLXXXXXXXXXXXXXXXXXNTYVYVXXXXXXXXXXXXXXXXXQFAALKTTAANTTDETAG 478
NL V+ A+ AG
Sbjct: 375 ETTVNLRDVTGNFNANVKSASGANYNAVI-----ASGNQSLGAG 413

Query: 479 VTTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVD 538
VTTL+GAM V+DIAE+A+ LD++R+D+GS+QNQ+ ST+NNI++TQVNVKAAESQIRDVD
Sbjct: 414 VTTLRGAMVVIDIAESAMKMLDKVRS DLG SVQNQMISTVNNISITQVNVKAAESQIRDVD 473

Query: 539 FASESANYSKANILAQSGSYAMAQANSSQQNVLRLL 574
FA ESAN++K NILAQSGSYAM+QAN+ QQN+LRLL
Sbjct: 474 FAEESANFNKNNILAQSGSYAMSQANTVQQNLRLL 509

sp Q03843 **Flagellin A [flaA] [Helicobacter pylori (Campylobacter pylori)],** 509
FLAA_HELPY **Helicobacter pylori J99 (Campylobacter pylori J99)]** AA
align

Score = 438 bits (1126), Expect = e-121
Identities = 261/576 (45%), Positives = 345/576 (59%), Gaps = 72/576 (12%)

```

Query: 2   FRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLG 61
          F++NTN+ A+NA   S L   +L  SL RLSSGLRIN AADDASGM +ADSLRSQA++LG
Sbjct: 2   FQVNTNINAMNAHVQSALTQNALKTSLERLSSGLRINKAADDASGMTVADSLRSQASSLG 61

Query: 62  QAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDQGQSLKTRTMLQADINKLMEE 121
          QAI+N ND +GI+Q ADKAMDEQLKILDT+K KATQAAQDQGQ+ ++R  +Q+DI +L++
Sbjct: 62  QAIANTNDGMGIIQVADKAMDEQLKILDTVKVKATQAAQDQGQTTESRKAIQSDIVRLIQG 121

Query: 122 LDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSFT 181
          LDNI NTT++NG+ LLSG FTN+EFQ+GA SNQ++KA+IG+T S KIG  R  TGA
Sbjct: 122 LDNIGNTTTTYNGQALLSGQFTNKEFQVGAYSNQSIKASIGSTTSKIGQVRIATGALITA 181

Query: 182 SGVVGLTIKXNYGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVRATYDVKTGTGVY 241
          SG + LT K  +G+ D   ++V +S+S GTG+G LAE INK++++TGV+A   V TT
Sbjct: 182 SGDISLTFKQVDGVNDVTLESVKVSSAGTGIGVLAEVINKNSNRTGVKAYASVITTSDV 241

Query: 242 AIKEGTTSQDFAINGVTIGKI-EYKDGNGSLISAINAVKDTTGVQASKDENGKLVLTLS 300
          A++ G+ S +  +NG+ +G I + K  D +G L++AINAV  TGV+A  D+ G
Sbjct: 242 AVQSGSLS-NLTLNGIHLGNIADIKKNDSGRLVAAINAVTSETGVEAYTDQKG----- 294

Query: 301 ADGRGIKITGDIGVSGILANQKENYGRSLVKNDRDINISGTNLSAIGMGTTDMIS-- 358
          RL+L  DGR I I  ++S G      M++
Sbjct: 295 -----RLNLRSIDGRGIEIKTDSVSN-GPSALTMVNGG 326

Query: 359 QSSVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXX 418
          Q      + G++S T  DA              NV S S
Sbjct: 327 QDLTKGSTNYGRSLSLRLDAKSI-----NVVSASDSQHLGFTAIGFGESQVA 373

Query: 419 XXXKNLXXXXXXXXXXXXXXXXXXXXNTYVXXXXXXXXXXXXXXXXXQFAALKTTAANTTDETAG 478
          NL              V+              A+      +G
Sbjct: 374 ETTVNLRDVTGNFNANVKSASGANYNVAVI-----ASGNQSLGSG 412

Query: 479 VTTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVD 538
          VTTL+GAM V+DIAE+A+  LD++R+D+GS+QNQ+ ST+NNI++TQVNVKAAESQIRDVD
Sbjct: 413 VTTLRGAMVVIDIAESAMKMLDKVRSDLGSVQNQMISTVNNISITQVNVKAAESQIRDVD 472

Query: 539 FASESANYSKANILAQSGSYAMAQANSSQQNVLRLL 574
          FA ESAN++K NILAQSGSYAM+QAN+ QQN+LRLL
Sbjct: 473 FAEESANFNKNNILAQSGSYAMSQANTVQQNILRLL 508

```

tr Q8GD49 **Flagellin [flaB] [Helicobacter pylori (Campylobacter pylori)]** 514 AA

align

Score = 434 bits (1117), Expect = e-120

Identities = 275/587 (46%), Positives = 348/587 (58%), Gaps = 88/587 (14%)

```

Query: 2   FRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLG 61
          FRINTN+AAL + A   N + L +SL +LSSGLRIN AADD+SGMAIADSLRSQ+ LG
Sbjct: 3   FRINTNIAALTSHAVGVQNNRDLSSSLEKLSSGLRINKAADDSSGMAIADSLRSQSANLG 62

Query: 62  QAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDQGQSLKTRTMLQADINKLMEE 121
          QAI N NDA+G++QTADKAMDEQ+KILDTIKTKA QAAQDQGQ+L++R  LQ+DI +L+EE
Sbjct: 63  QAIRNANDAIGMVQTADKAMDEQIKILDTIKTKAVQAAQDQGQTLESRRALQSDIQRLL 122

```

```

Query: 122 LDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETG----- 176
          LDNIANTTSFNG+Q+LSG+F+N+EFQIGA SN TVKA+IG+T S KIG R ET
Sbjct: 123 LDNIANTTSFNGQQLSGSFSNKEFQIGAYSNTTVKASIGSTSSDKIGHVRMETSSFSGE 182

Query: 177 -----AQSFTSGVVGLTIKNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGV 229
          AQ+ T VGL K NG+ D+K + V ISTS GTG+GAL+E IN+ ++ GV
Sbjct: 183 GMLASAAQNLTE--VGLNFKQVNGVNDYKIETVRISTAGTGIGALSEIINRFSNTLGV 240

Query: 230 RATYDVKTTGVYAIKEGTTSDFAINGVTIGKI-EYKDGNGSLISAINAVKDTTGVQA 288
          RA+Y+V TG ++ GT ++ INGV IG + + D +G L +AIN+VK
Sbjct: 241 RASYNVMATGGTPVQSGTV-RELTINGVEIGTVNDVHKNDADGRLTNAINSVK----- 292

Query: 289 SKDENGKLVLTSAADGRGIKITGDIGVSGGILANQKENYGRSLVKNDGRDINISGTNLSA 348
          D G++ + DI GR++L DGR I++ + S
Sbjct: 293 -----DRTGVEASLDI-----QGRINLHSIDGRAISVHAASASG 326

Query: 349 IGMGTDDMISQSSVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXX 408
          G + S G+++ T ADA V N S +
Sbjct: 327 QVFGGNGFAGISGTQ-HAVIGRLTLTRADARDI-----IVSGVNFHSHVG----- 369

Query: 409 XXXXXXXXXXXXXXXKNLXXXXXXXXXXXXXXXXXXXXNTYVXXXXXXXXXXXXXXXXXQFAALKTT 468
          N V A
Sbjct: 370 -----FHSAQGVAEYTVNLRAVRGIFDANVASAAGANANGAQA 407

Query: 469 AANTTDETAGVTTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVK 528
          N+ AGVT+LKGAM VMD+A++A T LD+IR+D+GS+Q ++ +TINNI+VTQVNVK
Sbjct: 408 ETNSQGIGAGVTSKLGAMIVMDMADSARTQLDKIRSDMGSVQMELVTTINNISVTQVNVK 467

Query: 529 AAESQIRDVDFASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
          AAESQIRDVDFE ESAN+SK NILAQSGS+AMAQAN+ QQNVLRLLQ
Sbjct: 468 AAESQIRDVDFAEESANFSKYNILAQSGSFAMAQANAVQQNVLRLLQ 514

```

```

tr Q6VYQ2 Flagellin A [flaA] [Helicobacter pylori (Campylobacter 510
          pylori)] AA
          align

```

Score = 433 bits (1113), Expect = e-120

Identities = 259/576 (44%), Positives = 343/576 (58%), Gaps = 72/576 (12%)

```

Query: 2 FRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLG 61
          F++NTN+ A+NA S L +L SL RLSSGLRIN AADDASGM +ADSLRSQA++LG
Sbjct: 3 FQVNTNINAMNAHVQSALTQNALKTSLERLSSGLRINKAADDASGMTVADSLRSQASSLG 62

Query: 62 QAISNGNDALGILQTADKAMDEQLKILDITIKTKATQAAQDGQSLKTRTMLQADINKLMEE 121
          QAI+N ND +GI+Q ADKAMDEQLKIL T+K KATQAAQDGQ+ ++R +Q+DI +L++
Sbjct: 63 QAIAANTNDGMGIIQVADKAMDEQLKILYTVKVKATQAAQDGQTTESRKAIQSDIVRLIQG 122

Query: 122 LDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSFT 181
          LDNI NTT++NG+ LLSG FTN+EFQ+GA SNQ++KA+IG+T S KIG R TGA
Sbjct: 123 LDNIGNTTTTYNGQALLSGQFTNKEFQVGAYSNSQSIKASIGSTTSKIGQVRIATGALITA 182

Query: 182 SGVVGLTIKNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVRATYDVKTTGVY 241
          SG + LT K +G+ D ++V +S+S GTG+G LAE INK++++TGVA V TT
Sbjct: 183 SGDISLTFKQVDGVNDVTLESVKVSSSAGTGIGVLAEVINKNSNRTGVKAYASVITTSV 242

```

```
Query: 242 AIKEGTTSDFAINGVTIGKI-EYKGDGNGSLISAINAVKDTTGVQASKDENGKLV LTS 300
      A++ G+ S + +NG+ +G I + K D +G L++AINAV TGV+A D+ G
Sbjct: 243 AVQSGSLN-NLTNGIHLGNIADIKKNDSDGRLVAAINAVTSETGVEAYTDQKG----- 295

Query: 301 ADGRGIKITGDIGVSGILANQKENYGRSLVKN DGRDINISGTNLSAIGMGTTDMIS-- 358
      RL+L DGR I I ++S G M++
Sbjct: 296 -----RLNLRSIDGRGIEIKTDSVSN-GPSALTMVNGG 327

Query: 359 QSSVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXX 418
      Q + G++S T DA NV S S
Sbjct: 328 QDLTKGSTNYGRSLSLTRLDAKSI-----NVVSASDSQHLGFTAIGFGESQVA 374

Query: 419 XXXKNLXXXXXXXXXXXXXXXXXNTYVVXXXXXXXXXXXXXXXXXQFAALKTTAANTTDETAG 478
      NL V+ A+ +G
Sbjct: 375 ETTVNLRDVTGNFNANVKSASGANYNNAVI-----ASGNQSLGSG 413

Query: 479 VTTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVD 538
      VTTL+GAM V+DIAE+A+ LD++R+D+GS+QNQ+ ST+NNI++TQVNVKAAESQIRDVD
Sbjct: 414 VTTLRGAMVVIDIAESAMKMLDKVRSDLGSGVQNQMISTVNNISITQVNVKAAESQIRDVD 473

Query: 539 FASESANYSKANILAQSGSYAMAQANSSQQNVLRLL 574
      FA ESAN++K NIL QSGSYAM+QAN+ QQN+LRLL
Sbjct: 474 FAEESANFNKNNILQSGSYAMSQANTVQQNILRLL 509
```

tr Q84IC0 **Flagellin (Fragment) [flaA] [Campylobacter lari]** 487 AA
align

Score = 412 bits (1059), Expect = e-114

Identities = 214/305 (70%), Positives = 255/305 (83%), Gaps = 1/305 (0%)

```
Query: 1 GFRINTNVAALNAKANSDLNAKSLDASLRLSSGLRINSAADDASGMAIADSLRSQANTL 60
      GFRINTN A+LNA+ N+ +N+++LD+SL+RLSSGLRINSAADDASG+AIADSL++QAN+L
Sbjct: 1 GFRINTNGASLNAQVNAGMNSRALDSSSLARLSSGLRINSAADDASGLAIADSLKTQANSL 60

Query: 61 GQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLME 120
      GQAI+N NDA +LQ ADKAMDEQLKILDTIK KATQAAQDGQS KTR M+Q +INKLME
Sbjct: 61 GQAINNANDANSMLQIADKAMDEQLKILDTIKVKATQAAQDGQSAKTRAMIQGEINKLME 120

Query: 121 ELDNIANTTTFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSF 180
      ELDNIANTT++NGKQLLSG F+NQ+FQIG +NQT+ ATIGATQS+KIG TRFETG++
Sbjct: 121 ELDNIANTTTTYNGKQLLSGAFSNQQFQIGDKANQTINATIGATQSAKIGQTRFETGSRIT 180

Query: 181 TSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAE EINKSADKTGVRATYDVKT TGV 240
      SG G TIKNY+G+ DFK +V++STS GTGLGALA EINKS+DKTGVRAT V+T
Sbjct: 181 GSGNAGFTIKNYDGVNDFKIQSVILSTSAGTGLGALAE EINKSSDKTGVRATATVQTISS 240

Query: 241 YAIKEGTTSDFAINGVTIGKIEYKGDGNGSLISAINAVKDTTGVQASKDENGKLV LTS 300
      I+ G T F INGV IGK+ + GD +GSL++AINA KDTTGV+AS NG+LVL S
Sbjct: 241 GTIQAGNTGDTFTINGVVIGKVAQAGDKDGS LVAAINAKKDTTGVEASV-VNGQLVLNS 299

Query: 301 ADGRG 305
      ADGRG
Sbjct: 300 ADGRG 304
```

Score = 168 bits (426), Expect = 2e-40
Identities = 87/101 (86%), Positives = 97/101 (95%)

Query: 475 ETAGVTTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQI 534
++AGVTTL+GAMAVMDIA+TAI NLD IRA+IG+ QNQ+TSTINNI+VTQVNVKAAESQI
Sbjct: 387 QSAGVTTLQGAMAVMDIADTAIANLDTIRANIGATQNQITSTINNISVTQVNVKAAESQI 446

Query: 535 RDVDFASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ 575
RDVDFASESANYSKANILAQSGSYAMAQAN++ QNVLRLLQ
Sbjct: 447 RDVDFASESANYSKANILAQSGSYAMAQANAASQNVLRLLQ 487

tr Q8VN90 **Flagellin A (Fragment) [flaA] [Helicobacter pylori** 458
(Campylobacter AA
pylori)] align

Score = 383 bits (983), Expect = e-105
Identities = 233/531 (43%), Positives = 309/531 (57%), Gaps = 80/531 (15%)

Query: 34 GLRINSAADDASGMAIADSLRSQANTLGQAI SNGNDALGILQTADKAMDEQLKILDTIKT 93
GLRIN AADDASGM +ADSLRSQA++LGQAI+N ND +GI+Q ADKAMDEQLKILDT+K
Sbjct: 1 GLRINKAADDASGMTVADSLRSQASSLGQAIANTNDGMGIIQVADKAMDEQLKILDTVKV 60

Query: 94 KATQAAQDQGQSLKTRTMLQADINKLMEELDNIANTTSFNGKQLLSGNFTNQEFQIGASSN 153
KATQAAQDQGQ+ ++R +Q+DI +L++ LDNI NTT++NG+ LLSG FTN+EFQ+GA SN
Sbjct: 61 KATQAAQDQGQTTESRKAIQSDIVRLIQGLDNIGNTTTTYNGQALLSGQFTNKEFQVGAYSN 120

Query: 154 QTVKATIGATQSSKIGVTRFETGAQSFTSGVVGLTIKNGIEDFKFDNVVISTSVGTGL 213
Q++KA+IG+T S KIG R TGA SG + LT K +G+ D ++V +S+S GTG+
Sbjct: 121 QSIKASIGSTTSKIGQVRIATGALITASGDISLTFKQVDGVNDVTLESVKVSSSAGTGI 180

Query: 214 GALAEEINKSADKTGVRATYDVKTG VYAIKEGTT SQDFAINGVTIGKI-EYKGDGNGS 272
G LAE INK++++TGV+A V TT A++ G+ S + +NG+ +G I + K D +G
Sbjct: 181 GVLAEVINKNSNRTGVKAYASVITTS DVAVQSGSLS -NLTLNGIHLGNIADIKKNDSDGR 239

Query: 273 LISAINAVKDTTGVQASKDENGKLVLT SADGRGIKITGDIGVGSGILANQKENYGRLSLV 332
L++AINAV TGV+A D+ G RL+L
Sbjct: 240 LVAAINAVTSETGVEAYTDQKG-----RLNLR 266

Query: 333 KNDGRDINI-----SGTNLSAIGMGTTDMISQSSVSLRESKGQISATNADAMGFNSYKG 386
DGR I I +G N + G D+ S+ + G++S T DA
Sbjct: 267 SLDGRGIEIKTDSVSNP NATLTMVNGGQDLTKGST-----NYGRLSLTRLDAKSI----- 316

Query: 387 G GKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXXKNLXXXXXXXXXXXXXXXXXNTYV 446
NV S S NL V
Sbjct: 317 -----NVVSASDSQHLGFTAIGFGESQVAETTVNLRDVTGNFNANVKSASGANYNAV 368

Query: 447 VXXXXXXXXXXXXXQFAALKTTAANTTDETAGVTTLKGAMAVMDIAETAITNLDQIRADI 506
+ A+ +GVTTL+GAM V+DIAE+A+ LD++R+D+
Sbjct: 369 I-----ASGNQSLGSGVTTLRGAMVVIDIAESAMKMLDKVRS DL 407

Query: 507 GSIQNQVTSTINNITVTQVNVKAAESQIRDVDFASESANYSKANILAQSGS 557
GS+QNQ+ ST+NNI++TQVNVKAAESQIRDVDFA ESAN++K NILAQSGS
Sbjct: 408 GSVQNQMISTVNNISITQVNVKAAESQIRDVDFAEESANFNKNNILAQSGS 458

```
tr Q8VN91 Flagellin A (Fragment) [flaA] [Helicobacter pylori 458
          (Campylobacter AA
          pylori)] align
```

Score = 382 bits (982), Expect = e-105

Identities = 232/527 (44%), Positives = 308/527 (58%), Gaps = 72/527 (13%)

```
Query: 34  GLRINSAADDASGMAIADSLRSQANTLGQAISNGNDALGILQTADKAMDEQLKILDTIKT 93
          GLRIN AADDASGM +ADSLRSQA++LGQAI+N ND +GI+Q ADKAMDEQLKILDT+K
Sbjct: 1   GLRINKAADDASGMTVADSLRSQASSLGQAIAANTNDGMGIIQVADKAMDEQLKILDTVKV 60

Query: 94  KATQAAQDGQSLKTRTMLQADINKLMEELDNIANTTSFNGKQLLSGNFTNQEFQIGASSN 153
          KATQAAQDGQ+ ++R +Q+DI +L++ LDNI NTT++NG+ LLSG FTN+EFQ+GA SN
Sbjct: 61  KATQAAQDGQTTESRKAIQSDIVRLIQLLDNIGNTTTTYNGQALLSGQFTNKEFQVGAYSN 120

Query: 154 QTVKATIGATQSSKIGVTRFETGAQSFTSGVVGLTIKNGIEDFKFDNVVISTSVGTGL 213
          Q++KA+IG+T S KIG R TGA SG + LT K +G+ D ++V +S+S GTG+
Sbjct: 121 QSIKASIGSTTSKIGQVRIATGALITASGDISLTFKQVDGVNDVTLESVKVSSSAGTGI 180

Query: 214 GALAEEINKSADKTGVRATYDVKTGTGVYAIKEGTTSDFAINGVTIGKI-EYKDGDNNGS 272
          G LAE INK++++TGV+A V TT A++ G+ S + +NG+ +G I + K D +G
Sbjct: 181 GVLAEVINKNSNRTGVKAYASVITTSADVAVQSGSLN-NLTLNGIHLGNIADIKKNSDGR 239

Query: 273 LISAINAVKDTTGVQASKDENGKLVLTSDAGRGIKITGDIGVSGILANQKENYGRSLSV 332
          L++AINAV TGV+A D+ G RL+L
Sbjct: 240 LVAAINAVTSETGVEAYTDQKG-----RLNLR 266

Query: 333 KNDGRDINISGTNLSAIGMGTTDMIS--QSSVSLRESKGQISATNADAMGFNSYKGGGKF 390
          DGR I I ++S G M++ Q + G++S T DA
Sbjct: 267 SLDGRGIEIKTDSVSN-GPSALTMVNGGQDLTKGSTNYGRSLSLRLDAKSI----- 316

Query: 391 VFTQNVSSISAFMXXXXXXXXXXXXXXXXXXXXKNLXXXXXXXXXXXXXXXXXXXXNTYVVXXX 450
          NV S S NL V+
Sbjct: 317 ----NVVSASDSQHLGFTAIGFGESQVAETTVNLRDVTGNFNANVKSASGANYNVAVI--- 369

Query: 451 XXXXXXXXXXXXQFAALKTTAANTTDETAGVTTLKGAMAVMDIAETAITNLDQIRADIGSIQ 510
          A+ +GVTTL+GAM V+DIAE+A+ LD++R+D+GS+Q
Sbjct: 370 -----ASGNQSLGSGVTTLRGAMVVIDIAESAMKMLDKVRSDLGSVQ 411

Query: 511 NQVTSTINNITVTQVNVKAAESQIRDVDFASESANYSKANILAQSGS 557
          NQ+ ST+NNI++TQVNVKAAESQIRDVDFE SAN++K NILAQSGS
Sbjct: 412 NQMISTVNNISITQVNVKAAESQIRDVDFAEESANFNKNILAQSGS 458
```

```
tr Q8VLN3 Flagellin A (Fragment) [flaA] [Helicobacter pylori 458
          (Campylobacter AA
          pylori)] align
```

Score = 382 bits (982), Expect = e-105

Identities = 232/527 (44%), Positives = 308/527 (58%), Gaps = 72/527 (13%)

```
Query: 34  GLRINSAADDASGMAIADSLRSQANTLGQAISNGNDALGILQTADKAMDEQLKILDTIKT 93
          GLRIN AADDASGM +ADSLRSQA++LGQAI+N ND +GI+Q ADKAMDEQLKILDT+K
Sbjct: 1   GLRINKAADDASGMTVADSLRSQASSLGQAIAANTNDGMGIIQVADKAMDEQLKILDTVKV 60

Query: 94  KATQAAQDGQSLKTRTMLQADINKLMEELDNIANTTSFNGKQLLSGNFTNQEFQIGASSN 153
          KATQAAQDGQ+ ++R +Q+DI +L++ LDNI NTT++NG+ LLSG FTN+EFQ+GA SN
```

```

Sbjct: 61 KATQAAQDGQTTERKAIQSDIVRLIQGLDNIGNTTTTYNGQALLSGQFTNKEFQVGAYSN 120

Query: 154 QTVKATIGATQSSKIGVTRFETGAQSFTSGVVGLTIKNGIEDFKFDNVVISTSVGTGL 213
          Q++KA+IG+T S KIG R TGA SG + LT K +G+ D ++V +S+S GTG+
Sbjct: 121 QSIKASIGSTTSKIGQVRIATGALITASGDISLTFKQVDGVNDVTLESVKVSSSAGTGI 180

Query: 214 GALAEEINKSADKTGVRATYDVKTGTGVYAIKEGTTSDQFAINGVTIGKI-EYKGDGNGS 272
          G LAE INK++++TGV+A V TT A++ G+ S + +NG+ +G I + K D +G
Sbjct: 181 GVLAEVINKNSNRTGVKAYASVITTSADVAVQSGSLS-NLTLNGIHLGNIADIKKNDSDGR 239

Query: 273 LISAINAVKDTTGVQASKDENGKLVLTSDAGRGIKITGDIGVSGILANQKENYGRSLV 332
          L++AINAV TGV+A D+ G RL+L
Sbjct: 240 LVAAINAVTSETGVEAYTDQKG-----RLNLR 266

Query: 333 KNDGRDINISGTNLSAIGMGTTDMIS--QSSVSLRESKGQISATNADAMGFNSYKGGGKF 390
          DGR I I ++S G M++ Q + G++S T DA
Sbjct: 267 SIDGRGIEIKTDSVSN-GPSALTMVNGGQDLTKGSTNYGRSLSLTRLDAKSI----- 316

Query: 391 VFTQNVSSISAFMXXXXXXXXXXXXXXXXXXXXKNLXXXXXXXXXXXXXXXXXXXXNTYVVXXX 450
          NV S S NL V+
Sbjct: 317 ----NVVSASDSQHLGFTAIGFGESQVAETTVNLRDVTGNFNANVKSASGANYNAVI--- 369

Query: 451 XXXXXXXXXXXQFAALKTTAANTTDETAGVTTLLKGAMAVMDIAETAITNLDQIRADIGSIQ 510
          A+ +GVTTL+GAM V+DIAE+A+ LD++R+D+GS+Q
Sbjct: 370 -----ASGNQSLSGSVTTLRGAMVVIDIAESAMKMLDKVRSDLGSGV 411

Query: 511 NQVTSTINNITVTQVNVKAAESQIRDVDFASESANYSKANILAQSGS 557
          NQ+ ST+NNI++TQVNVKAAESQIRDVDFA ESAN++K NILAQSGS
Sbjct: 412 NQMISTVNNISITQVNVKAAESQIRDVDFAEESANFNKNNILAQSGS 458

```

```

sp Q07910      Flagellin B (Flagellin N) [flaB] [Helicobacter mustelae] 513 AA
   FLAB_HELMU

```

[align](#)

Score = 381 bits (978), Expect = e-104

Identities = 216/405 (53%), Positives = 275/405 (67%), Gaps = 24/405 (5%)

```

Query: 2 FRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLG 61
          FRINTN+AALNA + +++ SL +LSSGLRIN AADDASGMAIADSLRSQ+ +LG
Sbjct: 2 FRINTNIAALNAHSIGVQTNRNIAAGSLEKLSSGLRINKAADDASGMAIADSLRSQSESLG 61

Query: 62 QAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLMEE 121
          QA+ N NDA+G++Q ADKAMDEQLKILDTIK KA QAAQDGQS ++R LQ+DI +LMEE
Sbjct: 62 QAVRNANDAIGMIQIADKAMDEQLKILDTIKAKAIQAAQDGQSQESRRSLQSDIRRLMEE 121

Query: 122 LDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFET----- 175
          LDNIANTTSFNG+Q+LSG FTN+EFQIGA SN TVKA+IG T S KIG R ET
Sbjct: 122 LDNIANTTSFNGQQLSGAFTNKEFQIGAYSNTTVKASIGPTSSDKIGHIRMETASFSGV 181

Query: 176 -----GAQSFTSGVVGLTIKNGIEDFKFDNVVISTSVGTGLGALAEEINKSADKTGV 229
          G + T V L K +G+ F+ +NV ISTS GTG+GAL+E IN+ +DK G+
Sbjct: 182 GMLASAGGNNLTE--VALNFKATDGVNSFELENVRISTSAGTGIGALSEVINRFSDKLG 239

Query: 230 RATYDVKTGTGVYAIKEGTTSDQFAINGVTIGKI-EYKGDGNGSLISAINAVKDTTGVQA 288
          RATY+V TG + GT + INGV IG + E + D +G LI+AIN+VK+ TGV+A

```


Sbjct: 240 RATYNVMATGTSPVMSGTV-RGLVINGVRIGTVNEVRKNDS DGR LINAINS VKNQ TGVEA 298

Query: 289 SKDENGKLVLT SADGRGIKITGD-----IGVG--SGILANQKENYGR LSLVKNDGRDIN 340
 S D G++ L S DGR I + D G G +GI N GRL+L++ D RDI

Sbjct: 299 SLDITGRINLVSLDGRAISVHADGEASHVFEGENFTGISGNNHAIVGRLTLIRTDARDII 358

Query: 341 ISGTNLSAIGMGTTDMISQSSVSLRESKGQISATNADAMGFNSYK 385
 +SG N S IG+ + +++++ +LR+ +G A A A G N+ K

Sbjct: 359 VSGVNFSHIGLHSAQGVAETTANLRQLRGMFGADIASAAGANANK 403

tr Q7X2D0 **Flagellin B [flaB] [Helicobacter pylori (Campylobacter pylori)]** 514 AA align

Score = 380 bits (976), Expect = e-104
 Identities = 216/403 (53%), Positives = 278/403 (68%), Gaps = 24/403 (5%)

Query: 2 FRINTNVAALNAKANS DLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLG 61
 FRINTN+AAL + A N + L +SL +LSSGLRIN AADD+SGMAIADSLRSQ+ LG

Sbjct: 3 FRINTNIAALTSHAVGVQNNRDLSSSLEKLSSGLRINKAADDSSGMAIADSLRSQSANLG 62

Query: 62 QAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLMEE 121
 QAI N NDA+G++QTADKAMDEQ+KILDTIKTKA QAAQDGQ+L++R LQ+DI +L+EE

Sbjct: 63 QAIRNANDAIGMVQTADKAMDEQIKILDTIKTKAVQAAQDGQTLESRKALQSDIQRLEE 122

Query: 122 LDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFET----- 175
 LDNIANTTSFNG+Q+LSG+F+N+EFQIGA SN TVKA+IG+T S KIG R ET

Sbjct: 123 LDNIANTTSFNGQQMLSGSFSNKEFQIGAYSNTTVKASIGSTSSDKIGHVRMETSSFSAE 182

Query: 176 -----GAQSFTSGVVGLTIKNGYNGIEDFKFDNVVISTSVGTGLGALAE EINKSADKTGV 229
 AQ+ T VGL K NG+ D+K + V ISTS GTG+GAL+E IN+ ++ GV

Sbjct: 183 GMLASAAAQNLTE--VGLNFKQVNGVNDYKIETVRIST SAGTGIGALSEIINRFSNTLG 240

Query: 230 RATYDVKTTGVYAIKEGTT SQDFAINGVTIGKI-EYKDG DNGSLISAINAVKDTTGVQA 288
 RA+Y+V TG ++ GT +D INGV IG + + D +G LI+AIN+VKD TGV+A

Sbjct: 241 RASYNVMATGGTPVQSGTV-KDLTINGVEIGTVNDVHKNDADGR LINAINS VKDR TGVEA 299

Query: 289 SKDENGKLVLT SADGRGIKI-----TGDI---GVSGILANQKENYGR LSLVKNDGRDIN 340
 S D G++ L S DGR I + +G + G +GI Q GRL+L + D RDI

Sbjct: 300 SLDIQGRINLH SIDGRAISVHATSASGQVFGGNGFAGISGTQHAVIGRLTLTRTDARDII 359

Query: 341 ISGTNLSAIGMGTTDMISQSSVSLRESKGQISATNADAMGFNS 383
 +SG N S +G + +++ +V+LR +G A A A G N+

Sbjct: 360 VSGVNFSHVG FHS AQGVAEYTVNLRAVRGIFDANVASAAGANA 402

tr Q8RNU8 **Flagellin B subunit [flaB] [Helicobacter pylori (Campylobacter pylori)]** 514 AA align

Score = 378 bits (970), Expect = e-103
 Identities = 214/403 (53%), Positives = 278/403 (68%), Gaps = 24/403 (5%)

Query: 2 FRINTNVAALNAKANS DLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLG 61

```

Sbjct: 3  FRINTN+AAL + A      N + L +SL +LSSGLRIN AADD+SGMAIADSLRSQ+  LG
FRINTNIAALTSHAVGVQNNRDLSSSLEKLSSGLRINKAADDSSGMAIADSLRSQSANLG 62

Query: 62  QAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLMEE 121
QAI N NDA+G++QTADKAMDEQ+KILDTIKTKA QAAQDGQ+L++R  LQ+DI +L+EE
Sbjct: 63  QAIRNANDAIGMVQTADKAMDEQIKILDTIKTKAVQAAQDGQTLESRRALQSDIQRLLLE 122

Query: 122  LDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFET----- 175
LDNIANTTSFNG+Q+LSG+F+N+EFQIGA SN TVKA+IG+T S KIG  R ET
Sbjct: 123  LDNIANTTSFNGQQLSGSFSNKEFQIGAYSNTTVKASIGSTSSDKIGHVRMETSSFSGE 182

Query: 176  -----GAQSFTSGVVGLTIKNGYNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGV 229
AQ+ T   VGL  K  NG+ D+K + V ISTS GTG+GAL+E IN+ ++  GV
Sbjct: 183  GMLASAAAQNLTE--VGLNFKQVNGVNDYKIETVRISTAGTGIGALSEIINRFSNTLGV 240

Query: 230  RATYDVKTGTGVYAIKEGTTSQDFAINGVTIGKI-EYKGDGNGSLISAINAVKDTTGVQA 288
RA+Y+V  TG   ++ GT  ++  INGV IG + + +  D +G L +AIN+VKD TGV+A
Sbjct: 241  RASYNVMATGGTPVQSGTV-RELTINGVEIGTVNDVRKNDADGRLTNAINSVKDRTGVEA 299

Query: 289  SKDENGKLVLTSA DGRGIKI-----TGDI---GVGSGILANQKENYGRSLVKNDGRDIN 340
S D  G++ L S DGR I +      +G +   G +GI   Q   GRL+L + D RDI
Sbjct: 300  SLDIQGRINLHSIDGRAISVHAASASGQVFGGNGFAGISGTQHAVIGRLTLTRTDARDII 359

Query: 341  ISGTNLSAIGMGTTDMISQSSVSLRESKQISATNADAMGFNS 383
+SG N S +G  +   +++ +V+LR  +G   A   A A G N+
Sbjct: 360  VSGVNFVSHVGFHSAQGVAEYTVNLRVIRGIFDANVASAAGANA 402

```

sp Q07911 **Flagellin B (Flagellin N) [flaB] [Helicobacter pylori 513 AA**
FLAB_HELPHY (Campylobacter pylori)]

align

Score = 377 bits (967), Expect = e-103

Identities = 214/403 (53%), Positives = 277/403 (68%), Gaps = 24/403 (5%)

```

Query: 2  FRINTNVAALNAKANSDLNKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLG 61
FRINTN+AAL + A      N + L +SL +LSSGLRIN AADD+SGMAIADSLRSQ+  LG
Sbjct: 2  FRINTNIAALTSHAVGVQNNRDLSSSLEKLSSGLRINKAADDSSGMAIADSLRSQSANLG 61

Query: 62  QAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLMEE 121
QAI N NDA+G++QTADKAMDEQ+KILDTIKTKA QAAQDGQ+L++R  LQ+DI +L+EE
Sbjct: 62  QAIRNANDAIGMVQTADKAMDEQIKILDTIKTKAVQAAQDGQTLESRRALQSDIQRLLLE 121

Query: 122  LDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFET----- 175
LDNIANTTSFNG+Q+LSG+F+N+EFQIGA SN TVKA+IG+T S KIG  R ET
Sbjct: 122  LDNIANTTSFNGQQLSGSFSNKEFQIGAYSNTTVKASIGSTSSDKIGHVRMETSSFSGA 181

Query: 176  -----GAQSFTSGVVGLTIKNGYNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGV 229
AQ+ T   VGL  K  NG+ D+K + V ISTS GTG+GAL+E IN+ ++  GV
Sbjct: 182  GMLASAAAQNLTE--VGLNFKQVNGVNDYKIETVRISTAGTGIGALSEIINRFSNTLGV 239

Query: 230  RATYDVKTGTGVYAIKEGTTSQDFAINGVTIGKI-EYKGDGNGSLISAINAVKDTTGVQA 288
RA+Y+V  TG   ++ GT  ++  INGV IG + +   D +G L +AIN+VKD TGV+A
Sbjct: 240  RASYNVMATGGTPVQSGTV-RELTINGVEIGTVNDVHKNDADGRLTNAINSVKDRTGVEA 298

Query: 289  SKDENGKLVLTSA DGRGIKI-----TGDI---GVGSGILANQKENYGRSLVKNDGRDIN 340

```

```
      S D  G++ L S DGR I +      +G +   G  +GI   Q   GRL+L + D RDI
Sbjct: 299 SLDIQGRINLHSIDGRAISVHAASASGQVFGGGNFAGISGTQHAVIGRLTLTRTDARDII 358

Query: 341 ISGTNLSAIGMGTTDMISQSSVSLRESKGQISATNADAMGFNS 383
      +SG N S +G +      +++ +V+LR +G   A   A A G N+
Sbjct: 359 VSGVNFHSHVGFHSAQGVAEYTVNLRVAVRGIFDANVASAAGANA 401
```

sp Q9ZMV8 **Flagellin B (Flagellin N) [flaB] [Helicobacter pylori J99 513 AA**
FLAB_HELPJ **(Campylobacter pylori J99)]**

align

Score = 377 bits (967), Expect = e-103
Identities = 214/403 (53%), Positives = 277/403 (68%), Gaps = 24/403 (5%)

```
Query: 2   FRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLG 61
      FRINTN+AAL + A      N + L +SL +LSSGLRIN AADD+SGMAIADSLRSQ+ LG
Sbjct: 2   FRINTNIAALTSHAVGVQNNRDLSSSLEKLSSGLRINKAADDSSGMAIADSLRSQSANLG 61

Query: 62  QAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLMEE 121
      QAI N NDA+G++QTADKAMDEQ+KILDTIKTKA QAAQDGQ+L++R LQ+DI +L+EE
Sbjct: 62  QAIRNANDAIGMVQTADKAMDEQIKILDTIKTKAVQAAQDGQTLESRRALQSDIQRLEE 121

Query: 122 LDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFET----- 175
      LDNIANTTSFNG+Q+LSG+F+N+EFQIGA SN TVKA+IG+T S KIG R ET
Sbjct: 122 LDNIANTTSFNGQQMLSGSFSNKEFQIGAYSNTTVKASIGSTSSDKIGHVRMETSSFSGE 181

Query: 176 -----GAQSFTSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGV 229
      AQ+ T   VGL K NG+ D+K + V ISTS GTG+GAL+E IN+ ++ GV
Sbjct: 182 GMLASAAAQNLTE--VGLNFKQVNGVNDYKIETVRISTSGTGIGALSEIINRFSNTLGV 239

Query: 230 RATYDVKTGTGVYAIKEGTTSQDFAINGVTIGKI-EYKDGNGSLISAINAVKDTTGVQA 288
      RA+Y+V TG   ++ GT   ++ INGV IG + +   D +G L +AIN+VKD TGV+A
Sbjct: 240 RASYNVMATGGTPVQSGTV-RELTINGVEIGTVNDVHKNDADGRLTNAINSVKDRGTVEA 298

Query: 289 SKDENGKLVLTSA DGRGIKI-----TGDI---GVGSGILANQKENYGRLSLVKNDGRDIN 340
      S D  G++ L S DGR I +      +G +   G  +GI   Q   GRL+L + D RDI
Sbjct: 299 SLDIQGRINLHSIDGRAISVHAASASGQVFGGGNFAGISGTQHAVIGRLTLTRTDARDII 358

Query: 341 ISGTNLSAIGMGTTDMISQSSVSLRESKGQISATNADAMGFNS 383
      +SG N S +G +      +++ +V+LR +G   A   A A G N+
Sbjct: 359 VSGVNFHSHVGFHSAQGVAEYTVNLRVAVRGIFDANVASAAGANA 401
```

tr Q6VYQ1 **Flagellin B [flaB] [Helicobacter pylori (Campylobacter**
pylori)]

514
AA

align

Score = 377 bits (967), Expect = e-103
Identities = 214/403 (53%), Positives = 277/403 (68%), Gaps = 24/403 (5%)

```
Query: 2   FRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLG 61
      FRINTN+AAL + A      N + L +SL +LSSGLRIN AADD+SGMAIADSLRSQ+ LG
Sbjct: 3   FRINTNIAALTSHAVGVQNNRDLSSSLEKLSSGLRINKAADDSSGMAIADSLRSQSANLG 62
```

```

Query: 62  QAI SNNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLMEE 121
          QAI N NDA+G++QTADKAMDEQ+KILDTIKTKA QAAQDGQ+L++R LQ+DI +L+EE
Sbjct: 63  QAIRNANDAIGMVQTADKAMDEQIKILDTIKTKAVQAAQDGQTLESRRALQSDIQRLL 122

Query: 122 LDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFET----- 175
          LDNIANTTSFNG+Q+LSG+F+N+EFQIGA SN TVKA+IG+T S KIG R ET
Sbjct: 123 LDNIANTTSFNGQQMLSGSFSNKEFQIGAYSNTTVKASIGSTSSDKIGHVRMETSSFSGE 182

Query: 176 -----GAQSFTSGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEIINKSADKTGV 229
          AQ+ T VGL K NG+ D+K + V ISTS GTG+GAL+E IN+ ++ GV
Sbjct: 183 GMLASAAAQNLTE--VGLNFKQVNGVNDYKIETVRISTAGTGIGALSEIINRFSNTLGV 240

Query: 230 RATYDVKTGTGVYAIKEGTTSQDFAINGVTIGKI-EYKDGNGSLISAINAVKDTTGVQA 288
          RA+Y+V TG ++ GT ++ INGV IG + + D +G L +AIN+VKD TGV+A
Sbjct: 241 RASYNVMATGGTPVQSGTV-RELTINGVEIGTVNDVHKNDADGRLTNAINSVKDRTGVEA 299

Query: 289 SKDENGKLVLTSAADGRGIKI-----TGDI---GVGSGILANQKENYGRSLVKN DGRDIN 340
          S D G++ L S DGR I + +G + G +GI Q GRL+L + D RDI
Sbjct: 300 SLDIQGRINLHSDGRAISVHAASASQVFGGGNFAGISGTQHAVIGRLTLTRTDARDII 359

Query: 341 ISGTNLSAIGMGTTDMISQSSVSLRESKGQISATNADAMGFNS 383
          +SG N S +G + +++ +V+LR +G A A A G N+
Sbjct: 360 VSGVNFHSHVGFHSAQGVAEYTVNLRAVRGIFDANVASAAGANA 402

```

```

tr      Q9XB37      Flagellin B [flaB] [Helicobacter felis]      514 AA
                                align

```

Score = 373 bits (958), Expect = e-102
Identities = 250/576 (43%), Positives = 322/576 (55%), Gaps = 66/576 (11%)

```

Query: 2  FRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLG 61
          FRINTNVAALNA N + L SL +LSSGLRIN AADDASGMAIADSLRSQ+ +LG
Sbjct: 3  FRINTNVAALNAHTIGVRNNDRLSTSLEKLSSGLRINKAADDASGMAIADSLRSQSASLG 62

Query: 62  QAI SNNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLMEE 121
          QA+ N NDA+G++QTADKAMDEQ+KILDT+KTKA QAAQDGQ+ +TR LQ+DI +L+EE
Sbjct: 63  QAVRNANDAIGVVQTADKAMDEQIKILDTVKTAVQAAQDGQTAETRKALQSDILRLLEE 122

Query: 122 LDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSFT 181
          LDNIANTTSFNG+QLL+G+F+N+EFQIGA SN T+KA+IG T S KIG RFET A
Sbjct: 123 LDNIANTTSFNGQQLLAGSFSNKEFQIGAYSNTTIKASIGPTGSDKIGHVRFETSAM--- 179

Query: 182 SGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEIINKSADKTGVRATYDVKTGTGVY 241
          + G+E V G L E
Sbjct: 180 -----DRGGME-----VSAGAQNLEK-----TL 198

Query: 242 AIKEGTTSQDFAINGVTIGKIEYKDGNGSLISAINAVKDTTGVQASKDE--NGKLVLT 299
          K+ DF + V KI G G G+L++ IN T GV+A+ G+ +
Sbjct: 199 NFKQADAVNDFKLESV--KISTAGTGLGALVNVINKNSSTLGVRAVAVLGTGENSVE 255

Query: 300 SADGRGIKITGDIGVSGILANQKENYGRSLVKN DGRDINISGTNLSAIGMGTTDMISQ 359
          S G+ I G + +G+ + GRL+ N ++ T + A TD+ Q
Sbjct: 256 SGTINGLTINGVL-IGNVNDVQHNDRDGRLTNAINSVKE---RTGVEAY---TDI--Q 304

Query: 360 SSVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMXXXXXXXXXXXXXXXXX 419

```

```

      ++LR + G+ + +AD + + GG + N +I +
Sbjct: 305 GRINLRSTDGRAISVHADGKTGHVFGGNGFRGISGNAHAIVGRLTLTKENARDIIVS--- 361

Query: 420 XXXKNLXXXXXXXXXXXXXXXXXXNTYVXXXXXXXQFAALKTTAANTTDETAGV 479
      + N + A A N AGV
Sbjct: 362 ---GVNFSHVGLHSAQGVAEYTVNLQAIRGVFDANAASAGGGNANAAQAFNFKGIGAGV 418

Query: 480 TTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAESQIRDVDF 539
      T+L+GAM VMD+AE+A LD+IR+D+GS+Q ++ +TINNI+VTQVNVKAAESQIRDVDF
Sbjct: 419 TSLRGAMMVMDMAESARIQLDKIRSDLGSGVQMELVTTINNISVTQVNVKAAESQIRDVDF 478

Query: 540 ASESANYSKANILAQSGSYAMAQANSSQQNVRLRLQ 575
      A ESA++SK NILAQSGS+AMAQAN+ QQNVRLRLQ
Sbjct: 479 AEESASFSKFNILAQSGSFAMAQANAVQQNVRLRLQ 514

```

```

tr Q7TTM9 Major flagellin subunit FlaA_1 (Major flagellin subunit 508
      FlaA_2) AA
      [flaA_1] [Helicobacter hepaticus ATCC 51449] align

```

Score = 368 bits (944), Expect = e-100
 Identities = 206/395 (52%), Positives = 264/395 (66%), Gaps = 15/395 (3%)

```

Query: 2 FRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLG 61
      F++NTNV ALNA A S +L S+ +LSSGLRIN AADDASGMAIADSLRSQA+ LG
Sbjct: 3 FQVNTNVNALNAHAQSTFTQYNLKNSEKLSGLRINKAADDASGMAIADSLRSQASALG 62

Query: 62 QAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLMEE 121
      QAI N ND +GI+Q ADKAMDEQLKILDTIK+KA QAAQDGQS ++R+M+Q DI +L+E
Sbjct: 63 QAIRNTNDGMGIIQIADKAMDEQLKILDTIKSKAVQAAQDGQSTQSRSMIQMDIIRLIEG 122

Query: 122 LDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSFT 181
      LD+I N T++NG LLSG FTN+EFQ+GA SNQ++K +IG+T S KIG R ETGA
Sbjct: 123 LDSIGNNTTYNGMALLSGAFTNKEFQVGAYSNSIKTSIGSTTSKIGQVRIETGALVTA 182

Query: 182 SGVVGLTIKNYNGIEDFKFDNVVISTSVGTGLGALAEIINKSADKTGVRATYDVKTGTGVY 241
      SG V +T KN +G+ D ++V +S S GTGLG LAE INK++DKTGVRA + TT
Sbjct: 183 SGEVTVTFKNVDGVNDITLESVKVSHSAGTGLGVLAEVINKNSDKTGVRANAYTTSDE 242

Query: 242 AIKEGTTSDFAINGVTIGK-IEYKDGNGSLISAINAVKDTTGVQASKDENGKLVLTLS 300
      +IK G+ + + +NGV+IG I + D +G L+ A NA TGV+A D G+L+L S
Sbjct: 243 SIKSGSLA-NLMVNGVSIQDIIGIQKNDSDGRLVQAFNAATMHTGVEAYTDNLGRLMLRS 301

Query: 301 ADGRGIKITGDIGV-----GSGILANQKENYGRSLVKNDGRDINISGTNLS 347
      DGRGI + + V G L NYGRSLV+ D RDI +SG N+S
Sbjct: 302 TDGRGISLKANGAVPGQNDVAITTVNGGHDLTGANNYGRSLVVRTDARDIVVSGLNIS 361

Query: 348 AIGMGTTDMISQSSVSLRESKGQISATNADAMGFN 382
      + G ++Q++ +LR+ KG + A G N
Sbjct: 362 STGYNDTKVAQTTTNLRDMKGVFNENVRASGAN 396

```

```

tr Q7VF81 Minor flagellin subunit FlaB [flaB] [Helicobacter hepaticus] 514 AA
      align

```

sp P50612 **Flagellin A [flaA] [Helicobacter mustelae]** 494 AA
FLAA_HELMU align

Score = 345 bits (886), Expect = 1e-93
Identities = 204/406 (50%), Positives = 261/406 (64%), Gaps = 29/406 (7%)

Query: 2 FRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLG 61
F++NTN+ AL A + L SL +LSSGLRIN AADDASGM I+DSLRSQA+ LG
Sbjct: 2 FQVNTNINALTTSAGA--TQLGLKNSLEKLSSGLRINKAADDASGMTISDSLRSQASALG 59

Query: 62 QAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLMEE 121
QAISN ND +GI+Q ADKAMDEQLKILDTIK KATQAAQDGQSL++R +Q+DI +L++
Sbjct: 60 QAISNANDGIGIIQVADKAMDEQLKILDTIKVKATQAAQDGQSLSRKAIQSDIIRLIQ 119

Query: 122 LDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSFT 181
LDNI NTTN+NG+ LLSG +TN+EFQIG SNQ++K ++G+T S KIG R TGA
Sbjct: 120 LDNIGNTTSYNGQSLLSGQWTNKEFQIGTYSNQSIVSVGTTSDKIGQVRINTGAMITA 179

Query: 182 SGVVGLTIKNGYNGIEDFKFDNVVISTSVGTGLGALAEINKSADKTGVRATYDVKTTGVY 241
+ LT K NG + V IS SVGTGLG LAE INK++DKTG+RA V+TT
Sbjct: 180 ASEATLTFKQINGGGTSPLEGVKISHSVGTGLGVLAEVINKNSDKTGIRAKASVETTSK 239

Query: 242 AIKEGTTSQDFAINGVTIGKI-EYKDGNGSLISAINAVKDTTGVQASKDENGKLVLT 300
I G ++ IN V IG I + K GD +G L+ AINA+ +TGV+AS D G+L L S
Sbjct: 240 EIMSGNL-KNLTINDVNIGNIVDIKKGDADGRLVQAINALTSSTGVEASTDSKGRNLNLS 298

Query: 301 ADGRGIKITGD-----IGVSGILANQ-KENYGRSLSLVKNDRDINIS 342
DGRGI + D + G I + NYGRSLSLV+ D RDI ++
Sbjct: 299 VDGRGIVLKADASEDNGDGKSAPMAIDAVNGGQSITDGEAANYGRSLSLVRLDARDIVLT 358

Query: 343 GTN-----LSAIGMGTTDMISQSSVSLRESKGQISATNADAMGFN 382
++ SAIG G + ++ ++V+LR+ G+ A+ A G N
Sbjct: 359 SSDKPDENKFSAIGFGDNN-VAMATVNLRDVLGKFDASVKSASGAN 403

tr Q93NM1 **Flagellin A (Fragment) [flaA] [Campylobacter jejuni]** 194 AA
align

Score = 337 bits (864), Expect = 4e-91
Identities = 177/192 (92%), Positives = 185/192 (96%)

Query: 9 AALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLGQAISNGN 68
AALNAKAN+DLN+KSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLGQAISNGN
Sbjct: 1 AALNAKANADLNSKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLGQAISNGN 60

Query: 69 DALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLMEELDNIANT 128
DALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LMEELDNIANT
Sbjct: 61 DALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLMEELDNIANT 120

Query: 129 TSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSFTSGVVGLT 188
TSFNGKQLLSGNF NQEFQIGASSNQTVKATIGATQSSKIG+TRFETG + +SG V T
Sbjct: 121 TSFNGKQLLSGNFINQEFQIGASSNQTVKATIGATQSSKIGLTRFETGERISSSGEVQFT 180

Query: 189 IKNYNGIEDFKF 200
+KNYNGI+DFKF

Sbjct: 181 LKNYNGIDDFKF 192

tr Q93NM0 **Flagellin A (Fragment) [flaA] [Campylobacter jejuni]** 194 AA
align

Score = 337 bits (864), Expect = 4e-91
Identities = 176/192 (91%), Positives = 185/192 (95%)

Query: 9 AALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLGQAISNGN 68
AALNAKAN+DLN+KSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLGQAISNGN
Sbjct: 1 AALNAKANADLNSKSLDASLSRLSSGLRINSAADDASGMAIADSLRSQANTLGQAISNGN 60

Query: 69 DALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINKLMEELDNIANT 128
DALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADIN+LMEELDNIANT
Sbjct: 61 DALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQADINRLMEELDNIANT 120

Query: 129 TSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTRFETGAQSFTSGVVGLT 188
TSFNGKQLLSGNF NQEFQIGASSNQ+KATIGATQSSKIG+TRFETG + +SG V T
Sbjct: 121 TSFNGKQLLSGNFINQEFQIGASSNQTIKATIGATQSSKIGLTRFETGGRISSSGEVQFT 180

Query: 189 IKNYNGIEDFKF 200
+KNYNGI+DFKF
Sbjct: 181 LKNYNGIDDFKF 192

tr Q8VN93 **Flagellin B (Fragment) [flaB] [Helicobacter pylori** 461
(Campylobacter AA
pylori)] align

Score = 337 bits (863), Expect = 5e-91
Identities = 191/364 (52%), Positives = 249/364 (67%), Gaps = 24/364 (6%)

Query: 41 ADDASGMAIADSLRSQANTLGQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQ 100
ADD+SGMAIADSLRSQ+ LGQAI N NDA+G++QTADKAMDEQ+KILDTIKTKA QAAQ
Sbjct: 1 ADDSSGMAIADSLRSQSANLGQAIRNANDAIGMVQTADKAMDEQIKILDTIKTKAVQAAQ 60

Query: 101 DGQSLKTRTMLQADINKLMEELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATI 160
DGQ+L++R LQ+DI +L+EELDNIANTTSFNG+Q+LSG+F+N+EFQIGA SN TVKA+I
Sbjct: 61 DGQTLESRRALQSDIQRLLEELDNIANTTSFNGQQLSGSFSNKEFQIGAYSNTTVKASI 120

Query: 161 GATQSSKIGVTRFET-----GAQSFTSGVVGLTIKKNYNGIEDFKFDNVVISTS 208
G+T S KIG R ET AQ+ T VGL K NG+ D+K + V ISTS
Sbjct: 121 GSTSSDKIGHVRMETSSFSGEGMLASAAAQNLTE--VGLNFKQVNGVNDYKIETVRISTS 178

Query: 209 VGTGLGALABEINKSADKTGVRATYDVKTTGVYAIKEGTTSDFAINGVTIGKI-EYKDG 267
GTG+GAL+E IN+ ++ GVRA+Y+V TG ++ GT ++ INGV IG + +
Sbjct: 179 AGTGIGALSEIINRFSNTLGVRASYNVMATGGTPVQSGTV-RELTINGVEIGTVNDVHKN 237

Query: 268 DGNGLISAINAVKDDTTGVQASKDENGKLVLTSDAGRGIKI-----TGDI---GVGSGIL 319
D +G L +AIN+VKD TGV+AS D G++ L S DGR I + +G + G +GI
Sbjct: 238 DADGRLTNAINSVKDRTGVEASMDIQGRINLHSDGRAISVHAASASGQVFGGNGFAGIS 297

Query: 320 ANQKENYGRLSLVKNDGRDINISGTNLSAIGMGTDMISQSSVSLRESKGQISATNADAM 379
Q GRL+L + D RDI +SG N S +G + +++ +V+LR +G A A A

Sbjct: 298 GTQHAVIGRLTLTRTDARDIIVSGVNFHSHVGFHSAQGVAEYTVNLRVARGIFDANVASAA 357

Query: 380 GFNS 383
G N+

Sbjct: 358 GANA 361

Database: EXPASY/UniProt

Posted date: Aug 29, 2004 10:26 AM

Number of letters in database: 494,584,931

Number of sequences in database: 1,544,870

Lambda	K	H
0.309	0.125	0.322

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

length of query: 575

length of database: 494,584,931

effective HSP length: 129

effective length of query: 446

effective length of database: 295,296,701

effective search space: 131702328646

effective search space used: 131702328646

T: 11

A: 40

X1: 16 (7.1 bits)

X2: 38 (14.6 bits)

X3: 64 (24.7 bits)

S1: 42 (21.7 bits)

S2: 76 (33.9 bits)

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CLUSTAL FORMAT for T-COFFEE Version_1.37, CPU=0.24 sec, SCORE=26760, Nseq=2, Len=576

```

unk|VIRT9350|Blast_submission -GFRINTNVAALNAKANSDLNAKSLDASLSRLSSGLRINSAADDASGMIAIDS
tr|Q7X516 MGFRINTNIGALNAHANSVVNSNELDKSLSRLLSSGLRINSAADDASGMIAIDS
          *****:.****:*** :*:.** *****

unk|VIRT9350|Blast_submission LGQAISNGNDALGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQ
tr|Q7X516 LGQAINNGNDAIGILQTADKAMDEQLKILDTIKTKATQAAQDGQSLKTRTMLQ
          *****:*****

unk|VIRT9350|Blast_submission EELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTR
tr|Q7X516 EELDNIANTTSFNGKQLLSGNFTNQEFQIGASSNQTVKATIGATQSSKIGVTR
          *****

unk|VIRT9350|Blast_submission FTSGVVGLTIKYNNGIEDFKFDNVVISTSVGTGLGALAEIEINKSADKTGVRAT
tr|Q7X516 FTSGVVGLTIKYNNGIEDFKFDNVVISTSVGTGLGALAEIEINKSADKTGVRAT
          *****

unk|VIRT9350|Blast_submission VYAIKEGTTSQDFAINGVTIGKIEYKDGNGSLISAINAVKDDTTGVQASKDE
tr|Q7X516 VYAIKEGTTSQDFAINGVAIGQINYKDGDNNGQLVSAINAVKDDTTGVQASKDE
          *****:.*:.*:*****.*.*:*****

unk|VIRT9350|Blast_submission SADGRGIKITGDIGVSGILANQKENYGRSLVKNDGRDINISGTNLSAIGMG
tr|Q7X516 SADGRGIKITGDIGVSGILANQKENYGRSLVKNDGRDINISGTNLSAIGMG
          *****

unk|VIRT9350|Blast_submission SSVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMSAQSGGFSR
tr|Q7X516 SSVSLRESKGQISATNADAMGFNSYKGGGKFVFTQNVSSISAFMSAQSGGFSR
          *****

unk|VIRT9350|Blast_submission SGKNLSVGLSQGIQIISSAASMSNTYVVSAGSGFSSGSGNSQFAALKTTAANT
tr|Q7X516 SGKNLSVGLSQGIQIISSAASMSNTYVVSAGSGFSSGSGNSQFAALKTTAANT
          *****

unk|VIRT9350|Blast_submission TTLKGAMAVMDIAETAITNLDQIRADIGSIQNQVTSTINNITVTQVNVKAAES
tr|Q7X516 TTLKGAMAVMDIAETAITNLDQIRADIGSVQNQLQVTINNITVTQVNVKAAES
          *****:***: *****

unk|VIRT9350|Blast_submission ASESANYSKANILAQSGSYAMAQANSSQQNVLRLLQ
tr|Q7X516 ASESANFSKYNILAQSGSYAMSQANAVQQNVLKLQ
          *****:.* *****:***: *****:***

```